



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Murphy, Patricia  
White, Marga  
Olson, Sheri  
Yoshikawa, Matthew  
Jackson, Geoffrey  
Eskanderi, Tara  
Schryer, Brenda  
Park, Michael
- (ii) TITLE OF THE INVENTION: NOVEL CODING SEQUENCE HAPLOTYPES  
OF THE HUMAN BRCA2 GENE
- (iii) NUMBER OF SEQUENCES: 134
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Morgan, Lewis & Bockius LLP
  - (B) STREET: 1111 Pennsylvania Ave., NW
  - (C) CITY: Washington
  - (D) STATE: DC
  - (E) COUNTRY: USA
  - (F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 09/084,471
  - (B) FILING DATE: 22 May 1998
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/055,784
  - (B) FILING DATE: 15 August 1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/064,926
  - (B) FILING DATE: 07 November 1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/065,367
  - (B) FILING DATE: 12 November 1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 09/071,715
  - (B) FILING DATE: 01 May 1998
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Michael S. Tuscan
  - (B) REGISTRATION NUMBER: 43,210

RECEIVED  
DEC 04 2002  
TECH CENTER 1600/2900

(C) REFERENCE/DOCKET NUMBER: 44921-5058-01-US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 202-739-3000
- (B) TELEFAX: 202-739-3001

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 26...75
- (D) OTHER INFORMATION: Exon 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
AGGGATTTCG TTTGTTTTAT TTTAGTCCTG TTGTTCTACA ATGTACACAT GTAACACCAC 60
AAAGAGATAA GTCAGGTATG ATTAAAAACA ATGCTTTTTA TTCTT 105
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 29...210
- (D) OTHER INFORMATION: Exon 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
TTTTTGCTAA GTATTTATTC TTTGATAGAT TTAATTACAA GTCTTCAGAA TGCCAGAGAT 60
ATACAGGATA TGCGAATTAA GAAGAAACAA AGGCAACGCG TCTTTCCACA GCCAGGCAGT 120
CTGTATCTTG CAAAAACATC CACTCTGCCT CGAATCTCTC TGAAAGCAGC AGTAGGAGGC 180
CAAGTTCCTT CTGCGTGTTT TCATAAACAG GTATGTGT 218
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 34...221
- (D) OTHER INFORMATION: Exon 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

tttttctttt ttgtgtgtgt ttattttgtg tagctgtata cgtatggcgt ttctaaacat 60
tgcataaaaa ttaacagcaa aaatgcagag tcttttcagt ttcacactga agattatttt 120
ggtaaggaaa gtttatggac tggaaaagga atacagttgg ctgatgggtg atggctcata 180
ccctccaatg atggaaaggc tggaaaagaa gaattttata ggtactctat gcaaaaagat 240
tgtgtgttaa cttttatg                                     258

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC 60
TCTGCTGCGC CTCGGGTGTC TTTTGC GGCG GTGGGTCGCC GCCGGGAGAA GCGTGAGGGG 120
ACAGATTGTG TACCGGCGCG GTTTTGTGCA GCTTACTCCG GCCAAAAAAG AACTGCACCT 180
CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT 237
                                     Met Pro Ile
                                     1

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC 285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
    5              10              15

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT 333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu
20              25              30              35

TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA 381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu
              40              45              50

CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG 429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg
              55              60              65

AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG 477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu
              70              75              80

CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT 525

```

Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys	Glu	Leu	Asp	
85						90					95					
AAA	TTC	AAA	TTA	GAC	TTA	GGA	AGG	AAT	GTT	CCC	AAT	AGT	AGA	CAT	AAA	573
Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser	Arg	His	Lys	
100					105					110					115	
AGT	CTT	CGC	ACA	GTG	AAA	ACT	AAA	ATG	GAT	CAA	GCA	GAT	GAT	GTT	TCC	621
Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp	Asp	Val	Ser	
				120					125					130		
TGT	CCA	CTT	CTA	AAT	TCT	TGT	CTT	AGT	GAA	AGT	CCT	GTT	GTT	CTA	CAA	669
Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val	Val	Leu	Gln	
				135				140					145			
TGT	ACA	CAT	GTA	ACA	CCA	CAA	AGA	GAT	AAG	TCA	GTG	GTA	TGT	GGG	AGT	717
Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val	Cys	Gly	Ser	
		150					155					160				
TTG	TTT	CAT	ACA	CCA	AAG	TTT	GTG	AAG	GGT	CGT	CAG	ACA	CCA	AAA	CAT	765
Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr	Pro	Lys	His	
165						170					175					
ATT	TCT	GAA	AGT	CTA	GGA	GCT	GAG	GTG	GAT	CCT	GAT	ATG	TCT	TGG	TCA	813
Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met	Ser	Trp	Ser	
180					185					190					195	
AGT	TCT	TTA	GCT	ACA	CCA	CCC	ACC	CTT	AGT	TCT	ACT	GTG	CTC	ATA	GTC	861
Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val	Leu	Ile	Val	
				200					205					210		
AGA	AAT	GAA	GAA	GCA	TCT	GAA	ACT	GTA	TTT	CCT	CAT	GAT	ACT	ACT	GCT	909
Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp	Thr	Thr	Ala	
				215				220					225			
AAT	GTG	AAA	AGC	TAT	TTT	TCC	AAT	CAT	GAT	GAA	AGT	CTG	AAG	AAA	AAT	957
Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu	Lys	Lys	Asn	
		230					235					240				
GAT	AGA	TTT	ATC	GCT	TCT	GTG	ACA	GAC	AGT	GAA	AAC	ACA	AAT	CAA	AGA	1005
Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr	Asn	Gln	Arg	
		245				250					255					
GAA	GCT	GCA	AGT	CAT	GGA	TTT	GGA	AAA	ACA	TCA	GGG	AAT	TCA	TTT	AAA	1053
Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn	Ser	Phe	Lys	
260					265					270					275	
GTA	AAT	AGC	TGC	AAA	GAC	CAC	ATT	GGA	AAG	TCA	ATG	CCA	AAT	GTC	CTA	1101
Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro	Asn	Val	Leu	
				280					285					290		
GAA	GAT	GAA	GTA	TAT	GAA	ACA	GTT	GTA	GAT	ACC	TCT	GAA	GAA	GAT	AGT	1149
Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu	Glu	Asp	Ser	
				295				300					305			
TTT	TCA	TTA	TGT	TTT	TCT	AAA	TGT	AGA	ACA	AAA	AAT	CTA	CAA	AAA	GTA	1197
Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu	Gln	Lys	Val	



310	315	320	
AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp 325 330 335			1245
GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val 340 345 350 355			1293
TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala 360 365 370			1341
CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val 375 380 385			1389
GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu 390 395 400			1437
AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys 405 410 415			1485
GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg 420 425 430 435			1533
AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser 440 445 450			1581
CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys 455 460 465			1629
AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala 470 475 480			1677
GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln 485 490 495			1725
GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr 500 505 510 515			1773
TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys 520 525 530			1821
GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser 535 540 545			1869

CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG	1917
Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp	
550 555 560	
CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA	1965
Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu	
565 570 575	
ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT	2013
Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His	
580 585 590 595	
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA	2061
Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser	
600 605 610	
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA	2109
Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala	
615 620 625	
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG	2157
Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val	
630 635 640	
AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA	2205
Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu	
645 650 655	
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA	2253
Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr	
660 665 670 675	
TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA	2301
Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala	
680 685 690	
AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT	2349
Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp	
695 700 705	
TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC	2397
Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser	
710 715 720	
AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC	2445
Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His	
725 730 735	
CCA GTA CAA CAT TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC	2493
Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser	
740 745 750 755	
CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA	2541
Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu	
760 765 770	

ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA	2589
Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg	
775 780 785	
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT	2637
Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr	
790 795 800	
GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA	2685
Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln	
805 810 815	
GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA	2733
Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro	
820 825 830 835	
CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC	2781
Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe	
840 845 850	
AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT	2829
Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr	
855 860 865	
ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC	2877
Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe	
870 875 880	
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT	2925
Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn	
885 890 895	
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT	2973
Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr	
900 905 910 915	
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA	3021
Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly	
920 925 930	
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG	3069
Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu	
935 940 945	
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA	3117
Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile	
950 955 960	
AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA	3165
Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile	
965 970 975	
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA	3213
Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly	
980 985 990 995	
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA	3261

Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly	Gly	Ser	Phe	Arg	Thr		
				1000					1005					1010			
GCT	TCA	AAT	AAG	GAA	ATC	AAG	CTC	TCT	GAA	CAT	AAC	ATT	AAG	AAG	AGC	3309	
Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His	Asn	Ile	Lys	Lys	Ser		
			1015				1020					1025					
AAA	ATG	TTC	TTC	AAA	GAT	ATT	GAA	GAA	CAA	TAT	CCT	ACT	AGT	TTA	GCT	3357	
Lys	Met	Phe	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr	Pro	Thr	Ser	Leu	Ala		
			1030				1035					1040					
TGT	GTT	GAA	ATT	GTA	AAT	ACC	TTG	GCA	TTA	GAT	AAT	CAA	AAG	AAA	CTG	3405	
Cys	Val	Glu	Ile	Val	Asn	Thr	Leu	Ala	Leu	Asp	Asn	Gln	Lys	Lys	Leu		
			1045				1050					1055					
AGC	AAG	CCT	CAG	TCA	ATT	AAT	ACT	GTA	TCT	GCA	CAT	TTA	CAG	AGT	AGT	3453	
Ser	Lys	Pro	Gln	Ser	Ile	Asn	Thr	Val	Ser	Ala	His	Leu	Gln	Ser	Ser		
1060					1065					1070					1075		
GTA	GTT	GTT	TCT	GAT	TGT	AAA	AAT	AGT	CAT	ATA	ACC	CCT	CAG	ATG	TTA	3501	
Val	Val	Val	Ser	Asp	Cys	Lys	Asn	Ser	His	Ile	Thr	Pro	Gln	Met	Leu		
				1080					1085					1090			
TTT	TCC	AAG	CAG	GAT	TTT	AAT	TCA	AAC	CAT	AAT	TTA	ACA	CCT	AGC	CAA	3549	
Phe	Ser	Lys	Gln	Asp	Phe	Asn	Ser	Asn	His	Asn	Leu	Thr	Pro	Ser	Gln		
			1095					1100					1105				
AAG	GCA	GAA	ATT	ACA	GAA	CTT	TCT	ACT	ATA	TTA	GAA	GAA	TCA	GGA	AGT	3597	
Lys	Ala	Glu	Ile	Thr	Glu	Leu	Ser	Thr	Ile	Leu	Glu	Glu	Ser	Gly	Ser		
			1110				1115					1120					
CAG	TTT	GAA	TTT	ACT	CAG	TTT	AGA	AAA	CCA	AGC	TAC	ATA	TTG	CAG	AAG	3645	
Gln	Phe	Glu	Phe	Thr	Gln	Phe	Arg	Lys	Pro	Ser	Tyr	Ile	Leu	Gln	Lys		
			1125				1130				1135						
AGT	ACA	TTT	GAA	GTG	CCT	GAA	AAC	CAG	ATG	ACT	ATC	TTA	AAG	ACC	ACT	3693	
Ser	Thr	Phe	Glu	Val	Pro	Glu	Asn	Gln	Met	Thr	Ile	Leu	Lys	Thr	Thr		
1140					1145					1150					1155		
TCT	GAG	GAA	TGC	AGA	GAT	GCT	GAT	CTT	CAT	GTC	ATA	ATG	AAT	GCC	CCA	3741	
Ser	Glu	Glu	Cys	Arg	Asp	Ala	Asp	Leu	His	Val	Ile	Met	Asn	Ala	Pro		
				1160				1165					1170				
TCG	ATT	GGT	CAG	GTA	GAC	AGC	AGC	AAG	CAA	TTT	GAA	GGT	ACA	GTT	GAA	3789	
Ser	Ile	Gly	Gln	Val	Asp	Ser	Ser	Lys	Gln	Phe	Glu	Gly	Thr	Val	Glu		
			1175					1180					1185				
ATT	AAA	CGG	AAG	TTT	GCT	GGC	CTG	TTG	AAA	AAT	GAC	TGT	AAC	AAA	AGT	3837	
Ile	Lys	Arg	Lys	Phe	Ala	Gly	Leu	Lys	Asn	Asp	Cys	Asn	Lys	Ser			
			1190				1195				1200						
GCT	TCT	GGT	TAT	TTA	ACA	GAT	GAA	AAT	GAA	GTG	GGG	TTT	AGG	GGC	TTT	3885	
Ala	Ser	Gly	Tyr	Leu	Thr	Asp	Glu	Asn	Glu	Val	Gly	Phe	Arg	Gly	Phe		
			1205				1210				1215						
TAT	TCT	GCT	CAT	GGC	ACA	AAA	CTG	AAT	GTT	TCT	ACT	GAA	GCT	CTG	CAA	3933	
Tyr	Ser	Ala	His	Gly	Thr	Lys	Leu	Asn	Val	Ser	Thr	Glu	Ala	Leu	Gln		

1220	1225	1230	1235	
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT				3981
Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr	1240	1245	1250	
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT				4029
Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp	1255	1260	1265	
TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA				4077
Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val	1270	1275	1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA				4125
Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu	1285	1290	1295	
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA				4173
Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg	1300	1305	1310	1315
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT				4221
Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser	1320	1325	1330	
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT				4269
His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val	1335	1340	1345	
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC				4317
Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn	1350	1355	1360	
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG				4365
Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln	1365	1370	1375	
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT				4413
Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala	1380	1385	1390	1395
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT				4461
Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala	1400	1405	1410	
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT				4509
Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe	1415	1420	1425	
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT				4557
Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe	1430	1435	1440	
AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC				4605
Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn	1445	1450	1455	

TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG	4653
Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met	
1460 1465 1470 1475	
GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG	4701
Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu	
1480 1485 1490	
AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG	4749
Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln	
1495 1500 1505	
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT	4797
Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly	
1510 1515 1520	
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG	4845
Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu	
1525 1530 1535	
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA	4893
Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu	
1540 1545 1550 1555	
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG	4941
Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu	
1560 1565 1570	
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT	4989
Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala	
1575 1580 1585	
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC	5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn	
1590 1595 1600	
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT	5085
Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn	
1605 1610 1615	
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG	5133
Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu	
1620 1625 1630 1635	
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT	5181
Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro	
1640 1645 1650	
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA	5229
Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser	
1655 1660 1665	
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG	5277
Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln	
1670 1675 1680	

ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT	5325
Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp	
1685 1690 1695	
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG	5373
Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu	
1700 1705 1710 1715	
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT	5421
Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His	
1720 1725 1730	
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC	5469
Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn	
1735 1740 1745	
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC	5517
Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu	
1750 1755 1760	
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT	5565
Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val	
1765 1770 1775	
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA	5613
Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys	
1780 1785 1790 1795	
GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG	5661
Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu	
1800 1805 1810	
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT	5709
Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile	
1815 1820 1825	
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA	5757
Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala	
1830 1835 1840	
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT	5805
Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile	
1845 1850 1855	
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG	5853
Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys	
1860 1865 1870 1875	
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA	5901
Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala	
1880 1885 1890	
GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT	5949
Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser	
1895 1900 1905	
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC	5997

Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp	
1910	1915 1920
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG	6045
Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu	
1925	1930 1935
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA	6093
Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser	
1940	1945 1950 1955
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT	6141
Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser	
	1960 1965 1970
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG	6189
Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln	
	1975 1980 1985
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA	6237
Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile	
	1990 1995 2000
GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC	6285
Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn	
2005	2010 2015
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT	6333
Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr	
2020	2025 2030 2035
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT	6381
Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn	
	2040 2045 2050
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC	6429
Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Lys Val Ser	
	2055 2060 2065
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT	6477
Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe	
2070	2075 2080
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA	6525
Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg	
2085	2090 2095
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG	6573
Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu	
2100	2105 2110 2115
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA	6621
His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys	
	2120 2125 2130
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC	6669
Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His	



2135	2140	2145	
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln 2150 2155 2160			6717
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val 2165 2170 2175			6765
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly 2180 2185 2190 2195			6813
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val 2200 2205 2210			6861
TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala 2215 2220 2225			6909
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser 2230 2235 2240			6957
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn 2245 2250 2255			7005
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu 2260 2265 2270 2275			7053
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn 2280 2285 2290			7101
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser 2295 2300 2305			7149
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His 2310 2315 2320			7197
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys 2325 2330 2335			7245
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu 2340 2345 2350 2355			7293
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser 2360 2365 2370			7341

TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala 2375 2380 2385	7389
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr 2390 2395 2400	7437
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val 2405 2410 2415	7485
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln 2420 2425 2430 2435	7533
AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp 2440 2445 2450	7581
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala 2455 2460 2465	7629
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser 2470 2475 2480	7677
CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln 2485 2490 2495	7725
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr 2500 2505 2510 2515	7773
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val 2520 2525 2530	7821
CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys 2535 2540 2545	7869
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His 2550 2555 2560	7917
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile 2565 2570 2575	7965
CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala 2580 2585 2590 2595	8013

GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT	8061
Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp	
2600 2605 2610	
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC	8109
Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile	
2615 2620 2625	
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT	8157
Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala	
2630 2635 2640	
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA	8205
Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg	
2645 2650 2655	
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA	8253
Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile	
2660 2665 2670 2675	
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT	8301
Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser	
2680 2685 2690	
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA	8349
Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys	
2695 2700 2705	
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT	8397
Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp	
2710 2715 2720	
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC	8445
Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val	
2725 2730 2735	
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA	8493
Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly	
2740 2745 2750 2755	
GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA	8541
Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro	
2760 2765 2770	
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC	8589
Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg	
2775 2780 2785	
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG	8637
Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu	
2790 2795 2800	
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT	8685
Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp	
2805 2810 2815	
GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA	8733

Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser	
2820	2825 2830 2835
TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA	8781
Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala	
2840	2845 2850
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT	8829
Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr	
2855	2860 2865
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA	8877
Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro	
2870	2875 2880
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA	8925
Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln	
2885	2890 2895
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT	8973
Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala	
2900	2905 2910 2915
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT	9021
Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn	
2920	2925 2930
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA	9069
His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu	
2935	2940 2945
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA	9117
Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser	
2950	2955 2960
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA	9165
Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys	
2965	2970 2975
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT	9213
Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp	
2980	2985 2990 2995
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT	9261
Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu	
3000	3005 3010
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA	9309
Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu	
3015	3020 3025
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA	9357
Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu	
3030	3035 3040
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA	9405
Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys	

3045	3050	3055	
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA			9453
Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile			
3060	3065	3070	3075
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC			9501
Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val			
	3080	3085	3090
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA			9549
Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile			
	3095	3100	3105
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC			9597
Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser			
	3110	3115	3120
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT			9645
Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe			
	3125	3130	3135
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT			9693
Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe			
3140	3145	3150	3155
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA			9741
Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile			
	3160	3165	3170
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT			9789
Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn			
	3175	3180	3185
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC			9837
Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr			
	3190	3195	3200
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT			9885
Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser			
	3205	3210	3215
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC			9933
Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala			
3220	3225	3230	3235
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG			9981
Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys			
	3240	3245	3250
TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG			10029
Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys			
	3255	3260	3265
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT			10077
Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val			
	3270	3275	3280

AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG	10125
Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln	
3285 3290 3295	
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA	10173
Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys	
3300 3305 3310 3315	
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT	10221
Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile	
3320 3325 3330	
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA	10269
Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile	
3335 3340 3345	
AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA	10317
Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile	
3350 3355 3360	
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT	10365
Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr	
3365 3370 3375	
CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG	10413
Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu	
3380 3385 3390 3395	
AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA	10461
Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr	
3400 3405 3410	
ATT ACA ACT AAA AAA TAT ATC TAA	10485
Ile Thr Thr Lys Lys Tyr Ile	
3415	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys
1 5 10 15
Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
20 25 30
Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu
35 40 45

Glu	Ser	Glu	His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr	50	55	60
Pro	Gln	Arg	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile	65	70	75
Phe	Lys	Glu	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys	85	90	95
Glu	Leu	Asp	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser	100	105	110
Arg	His	Lys	Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp	115	120	125
Asp	Val	Ser	Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val	130	135	140
Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val	145	150	155
Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr	165	170	175
Pro	Lys	His	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met	180	185	190
Ser	Trp	Ser	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val	195	200	205
Leu	Ile	Val	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp	210	215	220
Thr	Thr	Ala	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu	225	230	235
Lys	Lys	Asn	Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr	245	250	255
Asn	Gln	Arg	Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn	260	265	270
Ser	Phe	Lys	Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro	275	280	285
Asn	Val	Leu	Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu	290	295	300
Glu	Asp	Ser	Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu	305	310	315
Gln	Lys	Val	Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala	325	330	335
Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr	340	345	350
Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser	355	360	365
Asn	Val	Ala	His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser	370	375	380
Lys	Glu	Val	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu	385	390	395
Ser	Gly	Leu	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile	405	410	415
Ser	Ser	Cys	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu	420	425	430
Asn	Lys	Arg	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg	435	440	445
Ile	Ser	Ser	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val	450	455	460
Val	Asn	Lys	Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys	465	470	475
Ile	Leu	Ala	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser	485	490	495
Ser	Phe	Gln	Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro			





Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser  
 965 970 975  
 Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys  
 980 985 990  
 Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser  
 995 1000 1005  
 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile  
 1010 1015 1020  
 Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr  
 1025 1030 1035 1040  
 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln  
 1045 1050 1055  
 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu  
 1060 1065 1070  
 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro  
 1075 1080 1085  
 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr  
 1090 1095 1100  
 Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu  
 1105 1110 1115 112  
 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile  
 1125 1130 1135  
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu  
 1140 1145 1150  
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met  
 1155 1160 1165  
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly  
 1170 1175 1180  
 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys  
 1185 1190 1195 1200  
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe  
 1205 1210 1215  
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu  
 1220 1225 1230  
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser  
 1235 1240 1245  
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys  
 1250 1255 1260  
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp  
 1265 1270 1275 1280  
 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn  
 1285 1290 1295  
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn  
 1300 1305 1310  
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser  
 1315 1320 1325  
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn  
 1330 1335 1340  
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp  
 1345 1350 1355 1360  
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly  
 1365 1370 1375  
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val  
 1380 1385 1390  
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln  
 1395 1400 1405  
 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser

1410	1415	1420
Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys		
1425	1430	1435
Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu		1440
	1445	1450
Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys		1455
	1460	1465
Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His		1470
	1475	1480
Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val		1485
	1490	1495
Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr		1500
1505	1510	1515
Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys		1520
	1525	1530
Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly		1535
	1540	1545
Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys		1550
	1555	1560
Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu		1565
	1570	1575
Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn		1580
1585	1590	1595
Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu		1600
	1605	1610
Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser		1615
	1620	1625
Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala		1630
	1635	1640
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile		1645
	1650	1655
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser		1660
1665	1670	1675
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly		1680
	1685	1690
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly		1695
	1700	1705
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp		1710
	1715	1720
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser		1725
	1730	1735
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser		1740
1745	1750	1755
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu		1760
	1765	1770
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser		1775
	1780	1785
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile		1790
	1795	1800
Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn		1805
	1810	1815
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly		1820
1825	1830	1835
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His		1840
	1845	1850
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys		1855
	1860	1865
		1870

Val	Ile	Lys	Glu	Asn	Asn	Glu	Asn	Lys	Ser	Lys	Ile	Cys	Gln	Thr	Lys	1875	1880	1885
Ile	Met	Ala	Gly	Cys	Tyr	Glu	Ala	Leu	Asp	Asp	Ser	Glu	Asp	Ile	Leu	1890	1895	1900
His	Asn	Ser	Leu	Asp	Asn	Asp	Glu	Cys	Ser	Thr	His	Ser	His	Lys	Val	1905	1910	1915
Phe	Ala	Asp	Ile	Gln	Ser	Glu	Glu	Ile	Leu	Gln	His	Asn	Gln	Asn	Met	1925	1930	1935
Ser	Gly	Leu	Glu	Lys	Val	Ser	Lys	Ile	Ser	Pro	Cys	Asp	Val	Ser	Leu	1940	1945	1950
Glu	Thr	Ser	Asp	Ile	Cys	Lys	Cys	Ser	Ile	Gly	Lys	Leu	His	Lys	Ser	1955	1960	1965
Val	Ser	Ser	Ala	Asn	Thr	Cys	Gly	Ile	Phe	Ser	Thr	Ala	Ser	Gly	Lys	1970	1975	1980
Ser	Val	Gln	Val	Ser	Asp	Ala	Ser	Leu	Gln	Asn	Ala	Arg	Gln	Val	Phe	1985	1990	1995
Ser	Glu	Ile	Glu	Asp	Ser	Thr	Lys	Gln	Val	Phe	Ser	Lys	Val	Leu	Phe	2005	2010	2015
Lys	Ser	Asn	Glu	His	Ser	Asp	Gln	Leu	Thr	Arg	Glu	Glu	Asn	Thr	Ala	2020	2025	2030
Ile	Arg	Thr	Pro	Glu	His	Leu	Ile	Ser	Gln	Lys	Gly	Phe	Ser	Tyr	Asn	2035	2040	2045
Val	Val	Asn	Ser	Ser	Ala	Phe	Ser	Gly	Phe	Ser	Thr	Ala	Ser	Gly	Lys	2050	2055	2060
Gln	Val	Ser	Ile	Leu	Glu	Ser	Ser	Leu	His	Lys	Val	Lys	Gly	Val	Leu	2065	2070	2075
Glu	Glu	Phe	Asp	Leu	Ile	Arg	Thr	Glu	His	Ser	Leu	His	Tyr	Ser	Pro	2085	2090	2095
Thr	Ser	Arg	Gln	Asn	Val	Ser	Lys	Ile	Leu	Pro	Arg	Val	Asp	Lys	Arg	2100	2105	2110
Asn	Pro	Glu	His	Cys	Val	Asn	Ser	Glu	Met	Glu	Lys	Thr	Cys	Ser	Lys	2115	2120	2125
Glu	Phe	Lys	Leu	Ser	Asn	Asn	Leu	Asn	Val	Glu	Gly	Gly	Ser	Ser	Glu	2130	2135	2140
Asn	Asn	His	Ser	Ile	Lys	Val	Ser	Pro	Tyr	Leu	Ser	Gln	Phe	Gln	Gln	2145	2150	2155
Asp	Lys	Gln	Gln	Leu	Val	Leu	Gly	Thr	Lys	Val	Ser	Leu	Val	Glu	Asn	2165	2170	2175
Ile	His	Val	Leu	Gly	Lys	Glu	Gln	Ala	Ser	Pro	Lys	Asn	Val	Lys	Met	2180	2185	2190
Glu	Ile	Gly	Lys	Thr	Glu	Thr	Phe	Ser	Asp	Val	Pro	Val	Lys	Thr	Asn	2195	2200	2205
Ile	Glu	Val	Cys	Ser	Thr	Tyr	Ser	Lys	Asp	Ser	Glu	Asn	Tyr	Phe	Glu	2210	2215	2220
Thr	Glu	Ala	Val	Glu	Ile	Ala	Lys	Ala	Phe	Met	Glu	Asp	Asp	Glu	Leu	2225	2230	2235
Thr	Asp	Ser	Lys	Leu	Pro	Ser	His	Ala	Thr	His	Ser	Leu	Phe	Thr	Cys	2245	2250	2255
Pro	Glu	Asn	Glu	Glu	Met	Val	Leu	Ser	Asn	Ser	Arg	Ile	Gly	Lys	Arg	2260	2265	2270
Arg	Gly	Glu	Pro	Leu	Ile	Leu	Val	Gly	Glu	Pro	Ser	Ile	Lys	Arg	Asn	2275	2280	2285
Leu	Leu	Asn	Glu	Phe	Asp	Arg	Ile	Ile	Glu	Asn	Gln	Glu	Lys	Ser	Leu	2290	2295	2300
Lys	Ala	Ser	Lys	Ser	Thr	Pro	Asp	Gly	Thr	Ile	Lys	Asp	Arg	Arg	Leu	2305	2310	2315
Phe	Met	His	His	Val	Ser	Leu	Glu	Pro	Ile	Thr	Cys	Val	Pro	Phe	Arg	2320		



Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro  
 2785 2790 2795 2800  
 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly  
 2805 2810 2815  
 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu  
 2820 2825 2830  
 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu  
 2835 2840 2845  
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala  
 2850 2855 2860  
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr  
 2865 2870 2875 2880  
 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg  
 2885 2890 2895  
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala  
 2900 2905 2910  
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala  
 2915 2920 2925  
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile  
 2930 2935 2940  
 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln  
 2945 2950 2955 2960  
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser  
 2965 2970 2975  
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro  
 2980 2985 2990  
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile  
 2995 3000 3005  
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn  
 3010 3015 3020  
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val  
 3025 3030 3035 3040  
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His  
 3045 3050 3055  
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val  
 3060 3065 3070  
 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala  
 3075 3080 3085  
 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys  
 3090 3095 3100  
 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile  
 3105 3110 3115 3120  
 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu  
 3125 3130 3135  
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu  
 3140 3145 3150  
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn  
 3155 3160 3165  
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu  
 3170 3175 3180  
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser  
 3185 3190 3195 3200  
 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu  
 3205 3210 3215  
 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu  
 3220 3225 3230  
 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met

3235					3240					3245					
Thr	Ser	Lys	Ser	Cys	Lys	Gly	Glu	Lys	Glu	Ile	Asp	Asp	Gln	Lys	Asn
3250					3255					3260					
Cys	Lys	Lys	Arg	Arg	Ala	Leu	Asp	Phe	Leu	Ser	Arg	Leu	Pro	Leu	Pro
3265					3270					3275					3280
Pro	Pro	Val	Ser	Pro	Ile	Cys	Thr	Phe	Val	Ser	Pro	Ala	Ala	Gln	Lys
3285					3290					3295					
Ala	Phe	Gln	Pro	Pro	Arg	Ser	Cys	Gly	Thr	Lys	Tyr	Glu	Thr	Pro	Ile
3300					3305					3310					
Lys	Lys	Lys	Glu	Leu	Asn	Ser	Pro	Gln	Met	Thr	Pro	Phe	Lys	Lys	Phe
3315					3320					3325					
Asn	Glu	Ile	Ser	Leu	Leu	Glu	Ser	Asn	Ser	Ile	Ala	Asp	Glu	Glu	Leu
3330					3335					3340					
Ala	Leu	Ile	Asn	Thr	Gln	Ala	Leu	Leu	Ser	Gly	Ser	Thr	Gly	Glu	Lys
3345					3350					3355					3360
Gln	Phe	Ile	Ser	Val	Ser	Glu	Ser	Thr	Arg	Thr	Ala	Pro	Thr	Ser	Ser
3365					3370					3375					
Glu	Asp	Tyr	Leu	Arg	Leu	Lys	Arg	Arg	Cys	Thr	Thr	Ser	Leu	Ile	Lys
3380					3385					3390					
Glu	Gln	Glu	Ser	Ser	Gln	Ala	Ser	Thr	Glu	Glu	Cys	Glu	Lys	Asn	Lys
3395					3400					3405					
Gln	Asp	Thr	Ile	Thr	Thr	Lys	Lys	Tyr	Ile						
3410					3415										

(2) INFORMATION FOR SEO ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 229...10482  
(D) OTHER INFORMATION: BRCA2 (OMI2)

(ix) FEATURE:

- (A) NAME/KEY: variation  
(B) LOCATION: 3624  
(D) OTHER INFORMATION: R = A or G. Xaa (amino acid position 1132) = Lys.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGTGGCGCGA	GCTTCTGAAA	CTAGGCGGCA	GAGGCGGAGC	CGCTGTGGCA	CTGCTGCGCC	60
TCTGCTGCGC	CTCGGGTGTC	TTTTGCGGCG	GTGGGTCGCC	GCCGGGAGAA	GCGTGAGGGG	120
ACAGATTTGT	GACCGGCGCG	GTTTTTGTCA	GCTTACTCCG	GCCAAAAAAG	AACTGCACCT	180
CTGGAGCGGA	CTTATTTACC	AAGCATTGGA	GGAATATCGT	AGGTAAAA	ATG CCT ATT	237
				Met Pro Ile		
				1		

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC 285  
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys  
5 10 15

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT	333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu	
20 25 30 35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA	381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	
40 45 50	
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG	429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	
55 60 65	
AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG	477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	
70 75 80	
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT	525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	
85 90 95	
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA	573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	
100 105 110 115	
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC	621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser	
120 125 130	
TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	
135 140 145	
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
150 155 160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
165 170 175	
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
180 185 190 195	
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	
200 205 210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	
215 220 225	
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
230 235 240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA	1005

Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr	Asn	Gln	Arg	
245						250					255					
GAA	GCT	GCA	AGT	CAT	GGA	TTT	GGA	AAA	ACA	TCA	GGG	AAT	TCA	TTT	AAA	1053
Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn	Ser	Phe	Lys	
260					265					270					275	
GTA	AAT	AGC	TGC	AAA	GAC	CAC	ATT	GGA	AAG	TCA	ATG	CCA	AAT	GTC	CTA	1101
Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro	Asn	Val	Leu	
				280					285					290		
GAA	GAT	GAA	GTA	TAT	GAA	ACA	GTT	GTA	GAT	ACC	TCT	GAA	GAA	GAT	AGT	1149
Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu	Glu	Asp	Ser	
			295					300					305			
TTT	TCA	TTA	TGT	TTT	TCT	AAA	TGT	AGA	ACA	AAA	AAT	CTA	CAA	AAA	GTA	1197
Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu	Gln	Lys	Val	
		310					315					320				
AGA	ACT	AGC	AAG	ACT	AGG	AAA	AAA	ATT	TTC	CAT	GAA	GCA	AAC	GCT	GAT	1245
Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala	Asn	Ala	Asp	
	325					330					335					
GAA	TGT	GAA	AAA	TCT	AAA	AAC	CAA	GTG	AAA	GAA	AAA	TAC	TCA	TTT	GTA	1293
Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr	Ser	Phe	Val	
340					345					350					355	
TCT	GAA	GTG	GAA	CCA	AAT	GAT	ACT	GAT	CCA	TTA	GAT	TCA	AAT	GTA	GCA	1341
Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser	Asn	Val	Ala	
				360					365					370		
CAT	CAG	AAG	CCC	TTT	GAG	AGT	GGA	AGT	GAC	AAA	ATC	TCC	AAG	GAA	GTT	1389
His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser	Lys	Glu	Val	
			375					380					385			
GTA	CCG	TCT	TTG	GCC	TGT	GAA	TGG	TCT	CAA	CTA	ACC	CTT	TCA	GGT	CTA	1437
Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu	Ser	Gly	Leu	
		390					395					400				
AAT	GGA	GCC	CAG	ATG	GAG	AAA	ATA	CCC	CTA	TTG	CAT	ATT	TCT	TCA	TGT	1485
Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile	Ser	Ser	Cys	
	405					410					415					
GAC	CAA	AAT	ATT	TCA	GAA	AAA	GAC	CTA	TTA	GAC	ACA	GAG	AAC	AAA	AGA	1533
Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu	Asn	Lys	Arg	
420					425					430					435	
AAG	AAA	GAT	TTT	CTT	ACT	TCA	GAG	AAT	TCT	TTG	CCA	CGT	ATT	TCT	AGC	1581
Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg	Ile	Ser	Ser	
				440					445					450		
CTA	CCA	AAA	TCA	GAG	AAG	CCA	TTA	AAT	GAG	GAA	ACA	GTG	GTA	AAT	AAG	1629
Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val	Val	Asn	Lys	
			455					460					465			
AGA	GAT	GAA	GAG	CAG	CAT	CTT	GAA	TCT	CAT	ACA	GAC	TGC	ATT	CTT	GCA	1677
Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys	Ile	Leu	Ala	



470					475					480							
GTA	AAG	CAG	GCA	ATA	TCT	GGA	ACT	TCT	CCA	GTG	GCT	TCT	TCA	TTT	CAG	1725	
Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser	Ser	Phe	Gln		
485					490					495							
GGT	ATC	AAA	AAG	TCT	ATA	TTC	AGA	ATA	AGA	GAA	TCA	CCT	AAA	GAG	ACT	1773	
Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro	Lys	Glu	Thr		
500					505					510					515		
TTC	AAT	GCA	AGT	TTT	TCA	GGT	CAT	ATG	ACT	GAT	CCA	AAC	TTT	AAA	AAA	1821	
Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn	Phe	Lys	Lys		
520					525					530							
GAA	ACT	GAA	GCC	TCT	GAA	AGT	GGA	CTG	GAA	ATA	CAT	ACT	GTT	TGC	TCA	1869	
Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr	Val	Cys	Ser		
535					540					545							
CAG	AAG	GAG	GAC	TCC	TTA	TGT	CCA	AAT	TTA	ATT	GAT	AAT	GGA	AGC	TGG	1917	
Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn	Gly	Ser	Trp		
550					555					560							
CCA	GCC	ACC	ACC	ACA	CAG	AAT	TCT	GTA	GCT	TTG	AAG	AAT	GCA	GGT	TTA	1965	
Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn	Ala	Gly	Leu		
565					570					575							
ATA	TCC	ACT	TTG	AAA	AAG	AAA	ACA	AAT	AAG	TTT	ATT	TAT	GCT	ATA	CAT	2013	
Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr	Ala	Ile	His		
580					585					590					595		
GAT	GAA	ACA	TCT	TAT	AAA	GGA	AAA	AAA	ATA	CCG	AAA	GAC	CAA	AAA	TCA	2061	
Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp	Gln	Lys	Ser		
600					605					610							
GAA	CTA	ATT	AAC	TGT	TCA	GCC	CAG	TTT	GAA	GCA	AAT	GCT	TTT	GAA	GCA	2109	
Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala	Phe	Glu	Ala		
615					620					625							
CCA	CTT	ACA	TTT	GCA	AAT	GCT	GAT	TCA	GGT	TTA	TTG	CAT	TCT	TCT	GTG	2157	
Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His	Ser	Ser	Val		
630					635					640							
AAA	AGA	AGC	TGT	TCA	CAG	AAT	GAT	TCT	GAA	GAA	CCA	ACT	TTG	TCC	TTA	2205	
Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr	Leu	Ser	Leu		
645					650					655							
ACT	AGC	TCT	TTT	GGG	ACA	ATT	CTG	AGG	AAA	TGT	TCT	AGA	AAT	GAA	ACA	2253	
Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg	Asn	Glu	Thr		
660					665					670					675		
TGT	TCT	AAT	AAT	ACA	GTA	ATC	TCT	CAG	GAT	CTT	GAT	TAT	AAA	GAA	GCA	2301	
Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr	Lys	Glu	Ala		
680					685					690							
AAA	TGT	AAT	AAG	GAA	AAA	CTA	CAG	TTA	TTT	ATT	ACC	CCA	GAA	GCT	GAT	2349	
Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro	Glu	Ala	Asp		
695					700					705							

TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC	2397
Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser	
710 715 720	
AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC	2445
Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His	
725 730 735	
CCA GTA CAA CAT TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC	2493
Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser	
740 745 750 755	
CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA	2541
Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu	
760 765 770	
ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA	2589
Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg	
775 780 785	
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT	2637
Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr	
790 795 800	
GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA	2685
Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln	
805 810 815	
GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA	2733
Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro	
820 825 830 835	
CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC	2781
Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe	
840 845 850	
AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT	2829
Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr	
855 860 865	
ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC	2877
Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe	
870 875 880	
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT	2925
Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn	
885 890 895	
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT	2973
Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr	
900 905 910 915	
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA	3021
Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly	
920 925 930	

GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu 935 940 945	3069
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile 950 955 960	3117
AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile 965 970 975	3165
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly 980 985 990 995	3213
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr 1000 1005 1010	3261
GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser 1015 1020 1025	3309
AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala 1030 1035 1040	3357
TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu 1045 1050 1055	3405
AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser 1060 1065 1070 1075	3453
GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu 1080 1085 1090	3501
TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln 1095 1100 1105	3549
AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser 1110 1115 1120	3597
CAG TTT GAA TTT ACT CAG TTT AGA AAR CCA AGC TAC ATA TTG CAG AAG Gln Phe Glu Phe Thr Gln Phe Arg Xaa Pro Ser Tyr Ile Leu Gln Lys 1125 1130 1135	3645
AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr 1140 1145 1150 1155	3693
TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA	3741

Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro	
1160 1165 1170	
TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA	3789
Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu	
1175 1180 1185	
ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT	3837
Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser	
1190 1195 1200	
GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT	3885
Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe	
1205 1210 1215	
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA	3933
Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln	
1220 1225 1230 1235	
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT	3981
Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr	
1240 1245 1250	
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT	4029
Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp	
1255 1260 1265	
TCT GTC GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA	4077
Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val	
1270 1275 1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA	4125
Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu	
1285 1290 1295	
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA	4173
Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg	
1300 1305 1310 1315	
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT	4221
Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser	
1320 1325 1330	
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT	4269
His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val	
1335 1340 1345	
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC	4317
Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn	
1350 1355 1360	
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG	4365
Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln	
1365 1370 1375	
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT	4413
Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala	

1380	1385	1390	1395	
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT				4461
Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala	1400	1405	1410	
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT				4509
Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe	1415	1420	1425	
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT				4557
Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe	1430	1435	1440	
AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC				4605
Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn	1445	1450	1455	
TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG				4653
Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met	1460	1465	1470	1475
GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG				4701
Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu	1480	1485	1490	
AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG				4749
Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln	1495	1500	1505	
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT				4797
Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly	1510	1515	1520	
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG				4845
Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu	1525	1530	1535	
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA				4893
Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu	1540	1545	1550	1555
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG				4941
Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu	1560	1565	1570	
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT				4989
Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala	1575	1580	1585	
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC				5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn	1590	1595	1600	
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT				5085
Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn	1605	1610	1615	

TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG	5133
Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu	
1620 1625 1630 1635	
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT	5181
Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro	
1640 1645 1650	
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA	5229
Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser	
1655 1660 1665	
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG	5277
Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln	
1670 1675 1680	
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT	5325
Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp	
1685 1690 1695	
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG	5373
Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu	
1700 1705 1710 1715	
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT	5421
Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His	
1720 1725 1730	
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC	5469
Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn	
1735 1740 1745	
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC	5517
Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu	
1750 1755 1760	
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT	5565
Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val	
1765 1770 1775	
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA	5613
Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys	
1780 1785 1790 1795	
GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG	5661
Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu	
1800 1805 1810	
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT	5709
Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile	
1815 1820 1825	
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA	5757
Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala	
1830 1835 1840	

TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT	5805
Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile	
1845 1850 1855	
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG	5853
Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys	
1860 1865 1870 1875	
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA	5901
Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala	
1880 1885 1890	
GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT	5949
Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser	
1895 1900 1905	
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC	5997
Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp	
1910 1915 1920	
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG	6045
Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu	
1925 1930 1935	
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA	6093
Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser	
1940 1945 1950 1955	
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT	6141
Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser	
1960 1965 1970	
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG	6189
Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln	
1975 1980 1985	
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA	6237
Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile	
1990 1995 2000	
GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC	6285
Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn	
2005 2010 2015	
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT	6333
Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr	
2020 2025 2030 2035	
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT	6381
Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn	
2040 2045 2050	
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC	6429
Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser	
2055 2060 2065	
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT	6477

Ile	Leu	Glu	Ser	Ser	Leu	His	Lys	Val	Lys	Gly	Val	Leu	Glu	Glu	Phe	
	2070						2075					2080				
GAT	TTA	ATC	AGA	ACT	GAG	CAT	AGT	CTT	CAC	TAT	TCA	CCT	ACG	TCT	AGA	6525
Asp	Leu	Ile	Arg	Thr	Glu	His	Ser	Leu	His	Tyr	Ser	Pro	Thr	Ser	Arg	
	2085					2090				2095						
CAA	AAT	GTA	TCA	AAA	ATA	CTT	CCT	CGT	GTT	GAT	AAG	AGA	AAC	CCA	GAG	6573
Gln	Asn	Val	Ser	Lys	Ile	Leu	Pro	Arg	Val	Asp	Lys	Arg	Asn	Pro	Glu	
2100					2105				2110					2115		
CAC	TGT	GTA	AAC	TCA	GAA	ATG	GAA	AAA	ACC	TGC	AGT	AAA	GAA	TTT	AAA	6621
His	Cys	Val	Asn	Ser	Glu	Met	Glu	Lys	Thr	Cys	Ser	Lys	Glu	Phe	Lys	
				2120				2125						2130		
TTA	TCA	AAT	AAC	TTA	AAT	GTT	GAA	GGT	GGT	TCT	TCA	GAA	AAT	AAT	CAC	6669
Leu	Ser	Asn	Asn	Leu	Asn	Val	Glu	Gly	Gly	Ser	Ser	Glu	Asn	Asn	His	
			2135				2140						2145			
TCT	ATT	AAA	GTT	TCT	CCA	TAT	CTC	TCT	CAA	TTT	CAA	CAA	GAC	AAA	CAA	6717
Ser	Ile	Lys	Val	Ser	Pro	Tyr	Leu	Ser	Gln	Phe	Gln	Gln	Asp	Lys	Gln	
	2150					2155				2160						
CAG	TTG	GTA	TTA	GGA	ACC	AAA	GTC	TCA	CTT	GTT	GAG	AAC	ATT	CAT	GTT	6765
Gln	Leu	Val	Leu	Gly	Thr	Lys	Val	Ser	Leu	Val	Glu	Asn	Ile	His	Val	
	2165				2170					2175						
TTG	GGA	AAA	GAA	CAG	GCT	TCA	CCT	AAA	AAC	GTA	AAA	ATG	GAA	ATT	GGT	6813
Leu	Gly	Lys	Glu	Gln	Ala	Ser	Pro	Lys	Asn	Val	Lys	Met	Glu	Ile	Gly	
2180				2185				2190					2195			
AAA	ACT	GAA	ACT	TTT	TCT	GAT	GTT	CCT	GTG	AAA	ACA	AAT	ATA	GAA	GTT	6861
Lys	Thr	Glu	Thr	Phe	Ser	Asp	Val	Pro	Val	Lys	Thr	Asn	Ile	Glu	Val	
				2200				2205					2210			
TGT	TCT	ACT	TAC	TCC	AAA	GAT	TCA	GAA	AAC	TAC	TTT	GAA	ACA	GAA	GCA	6909
Cys	Ser	Thr	Tyr	Ser	Lys	Asp	Ser	Glu	Asn	Tyr	Phe	Glu	Thr	Glu	Ala	
			2215				2220					2225				
GTA	GAA	ATT	GCT	AAA	GCT	TTT	ATG	GAA	GAT	GAT	GAA	CTG	ACA	GAT	TCT	6957
Val	Glu	Ile	Ala	Lys	Ala	Phe	Met	Glu	Asp	Asp	Glu	Leu	Thr	Asp	Ser	
	2230				2235					2240						
AAA	CTG	CCA	AGT	CAT	GCC	ACA	CAT	TCT	CTT	TTT	ACA	TGT	CCC	GAA	AAT	7005
Lys	Leu	Pro	Ser	His	Ala	Thr	His	Ser	Leu	Phe	Thr	Cys	Pro	Glu	Asn	
	2245				2250					2255						
GAG	GAA	ATG	GTT	TTG	TCA	AAT	TCA	AGA	ATT	GGA	AAA	AGA	AGA	GGA	GAG	7053
Glu	Glu	Met	Val	Leu	Ser	Asn	Ser	Arg	Ile	Gly	Lys	Arg	Arg	Gly	Glu	
2260				2265				2270						2275		
CCC	CTT	ATC	TTA	GTG	GGA	GAA	CCC	TCA	ATC	AAA	AGA	AAC	TTA	TTA	AAT	7101
Pro	Leu	Ile	Leu	Val	Gly	Glu	Pro	Ser	Ile	Lys	Arg	Asn	Leu	Leu	Asn	
			2280				2285						2290			
GAA	TTT	GAC	AGG	ATA	ATA	GAA	AAT	CAA	GAA	AAA	TCC	TTA	AAG	GCT	TCA	7149
Glu	Phe	Asp	Arg	Ile	Ile	Glu	Asn	Gln	Glu	Lys	Ser	Leu	Lys	Ala	Ser	



2295	2300	2305	
AAA AGC ACT CCA GAT GGC ACA ATA	AAA GAT CGA AGA TTG TTT ATG CAT		7197
Lys Ser Thr Pro Asp Gly Thr Ile	Lys Asp Arg Arg Leu Phe Met His		
2310	2315	2320	
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG			7245
His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys			
2325	2330	2335	
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA			7293
Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu			
2340	2345	2350	2355
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT			7341
Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser			
2360	2365	2370	
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT			7389
Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala			
2375	2380	2385	
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC			7437
Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr			
2390	2395	2400	
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT			7485
Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val			
2405	2410	2415	
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA			7533
Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln			
2420	2425	2430	2435
AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC			7581
Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp			
2440	2445	2450	
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT			7629
Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala			
2455	2460	2465	
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT			7677
Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser			
2470	2475	2480	
CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA			7725
Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln			
2485	2490	2495	
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA			7773
Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr			
2500	2505	2510	2515
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT			7821
Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val			
2520	2525	2530	

CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA	7869
Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys	
2535 2540 2545	
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC	7917
His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His	
2550 2555 2560	
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA	7965
Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile	
2565 2570 2575	
CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT	8013
Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala	
2580 2585 2590 2595	
GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT	8061
Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp	
2600 2605 2610	
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC	8109
Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile	
2615 2620 2625	
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT	8157
Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala	
2630 2635 2640	
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA	8205
Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg	
2645 2650 2655	
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA	8253
Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile	
2660 2665 2670 2675	
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT	8301
Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser	
2680 2685 2690	
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA	8349
Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys	
2695 2700 2705	
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT	8397
Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp	
2710 2715 2720	
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC	8445
Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val	
2725 2730 2735	
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA	8493
Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly	
2740 2745 2750 2755	

GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro 2760 2765 2770	8541
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg 2775 2780 2785	8589
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu 2790 2795 2800	8637
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp 2805 2810 2815	8685
GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser 2820 2825 2830 2835	8733
TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala 2840 2845 2850	8781
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr 2855 2860 2865	8829
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA Lys Ile Gln Glu Glu Phe Glu His Glu Glu Asn Thr Thr Lys Pro 2870 2875 2880	8877
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln 2885 2890 2895	8925
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala 2900 2905 2910 2915	8973
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn 2920 2925 2930	9021
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu 2935 2940 2945	9069
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser 2950 2955 2960	9117
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys 2965 2970 2975	9165
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT	9213

Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp	
2980	2985 2990 2995
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT	9261
Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu	
3000 3005 3010	
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA	9309
Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu	
3015 3020 3025	
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA	9357
Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu	
3030 3035 3040	
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA	9405
Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys	
3045 3050 3055	
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA	9453
Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile	
3060 3065 3070 3075	
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC	9501
Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val	
3080 3085 3090	
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA	9549
Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile	
3095 3100 3105	
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC	9597
Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser	
3110 3115 3120	
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT	9645
Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe	
3125 3130 3135	
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT	9693
Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe	
3140 3145 3150 3155	
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA	9741
Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile	
3160 3165 3170	
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT	9789
Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn	
3175 3180 3185	
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC	9837
Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr	
3190 3195 3200	
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT	9885
Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser	

3205	3210	3215	
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC			9933
Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala			
3220	3225	3230	3235
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG			9981
Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys			
	3240	3245	3250
TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG			10029
Ser Cys Lys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys			
	3255	3260	3265
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT			10077
Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val			
	3270	3275	3280
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG			10125
Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln			
	3285	3290	3295
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA			10173
Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys			
3300	3305	3310	3315
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT			10221
Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile			
	3320	3325	3330
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA			10269
Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile			
	3335	3340	3345
AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA			10317
Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile			
	3350	3355	3360
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT			10365
Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr			
	3365	3370	3375
CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG			10413
Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu			
3380	3385	3390	3395
AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA			10461
Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr			
	3400	3405	3410
ATT ACA ACT AAA AAA TAT ATC TAA			10485
Ile Thr Thr Lys Lys Tyr Ile			
	3415		

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3418 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:
  - (A) NAME/KEY: variation
  - (B) LOCATION: 1132
  - (D) OTHER INFORMATION: Xaa = Lys (from codon AAR,  
R = A or G).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys
 1           5           10           15
Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
          20           25           30
Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu
          35           40           45
Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
          50           55           60
Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
65           70           75           80
Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
          85           90           95
Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
          100          105          110
Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
          115          120          125
Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
          130          135          140
Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
145          150          155          160
Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
          165          170          175
Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
          180          185          190
Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
          195          200          205
Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
          210          215          220
Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
225          230          235          240
Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
          245          250          255
Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
          260          265          270
Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
          275          280          285
Asn Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
          290          295          300
Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
305          310          315          320
Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala

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Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr
			340					345					350		
Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser
		355					360					365			
Asn	Val	Ala	His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser
	370					375					380				
Lys	Glu	Val	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu
385					390					395					400
Ser	Gly	Leu	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile
			405					410						415	
Ser	Ser	Cys	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu
			420					425					430		
Asn	Lys	Arg	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg
		435					440					445			
Ile	Ser	Ser	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val
	450					455					460				
Val	Asn	Lys	Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys
465					470					475					480
Ile	Leu	Ala	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser
			485					490						495	
Ser	Phe	Gln	Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro
		500						505					510		
Lys	Glu	Thr	Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn
		515					520					525			
Phe	Lys	Lys	Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr
	530					535					540				
Val	Cys	Ser	Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn
545					550					555					560
Gly	Ser	Trp	Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn
			565					570						575	
Ala	Gly	Leu	Ile	Ser	Thr	Leu	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr	
		580						585				590			
Ala	Ile	His	Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp
		595					600					605			
Gln	Lys	Ser	Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala
	610					615					620				
Phe	Glu	Ala	Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His
625					630					635					640
Ser	Ser	Val	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr
			645					650						655	
Leu	Ser	Leu	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg
		660					665					670			
Asn	Glu	Thr	Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr
		675					680					685			
Lys	Glu	Ala	Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro
	690				695					700					
Glu	Ala	Asp	Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp
705					710					715					720
Pro	Lys	Ser	Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala
			725					730						735	
Ala	Cys	His	Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp
		740						745					750		
Phe	Gln	Ser	Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr
	755					760						765			
Leu	Ile	Leu	Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met
	770					775					780				

Ile	Ser	Arg	Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly	785	790	795	800
Asn	Asn	Tyr	Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu		805	810	815
Lys	Asn	Gln	Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu		820	825	830
Leu	Leu	Pro	Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys		835	840	845
Val	Gln	Phe	Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln		850	855	860
Glu	Glu	Thr	Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu		865	870	875
Glu	Leu	Phe	Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Val	Ala	Asn		885	890	895
Glu	Arg	Asn	Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu	Leu	His	Glu	Thr		900	905	910
Asp	Leu	Thr	Cys	Val	Asn	Glu	Pro	Ile	Phe	Lys	Asn	Ser	Thr	Met	Val		915	920	925
Leu	Tyr	Gly	Asp	Thr	Gly	Asp	Lys	Gln	Ala	Thr	Gln	Val	Ser	Ile	Lys		930	935	940
Lys	Asp	Leu	Val	Tyr	Val	Leu	Ala	Glu	Glu	Asn	Lys	Asn	Ser	Val	Lys		945	950	955
Gln	His	Ile	Lys	Met	Thr	Leu	Gly	Gln	Asp	Leu	Lys	Ser	Asp	Ile	Ser		965	970	975
Leu	Asn	Ile	Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asn	Lys		980	985	990
Trp	Ala	Gly	Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly	Gly	Ser		995	1000	1005
Phe	Arg	Thr	Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His	Asn	Ile		1010	1015	1020
Lys	Lys	Ser	Lys	Met	Phe	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr	Pro	Thr		1025	1030	1035
Ser	Leu	Ala	Cys	Val	Glu	Ile	Val	Asn	Thr	Leu	Ala	Leu	Asp	Asn	Gln		1045	1050	1055
Lys	Lys	Leu	Ser	Lys	Pro	Gln	Ser	Ile	Asn	Thr	Val	Ser	Ala	His	Leu		1060	1065	1070
Gln	Ser	Ser	Val	Val	Val	Ser	Asp	Cys	Lys	Asn	Ser	His	Ile	Thr	Pro		1075	1080	1085
Gln	Met	Leu	Phe	Ser	Lys	Gln	Asp	Phe	Asn	Ser	Asn	His	Asn	Leu	Thr		1090	1095	1100
Pro	Ser	Gln	Lys	Ala	Glu	Ile	Thr	Glu	Leu	Ser	Thr	Ile	Leu	Glu	Glu		1105	1110	1115
Ser	Gly	Ser	Gln	Phe	Glu	Phe	Thr	Gln	Phe	Arg	Xaa	Pro	Ser	Tyr	Ile		1125	1130	1135
Leu	Gln	Lys	Ser	Thr	Phe	Glu	Val	Pro	Glu	Asn	Gln	Met	Thr	Ile	Leu		1140	1145	1150
Lys	Thr	Thr	Ser	Glu	Glu	Cys	Arg	Asp	Ala	Asp	Leu	His	Val	Ile	Met		1155	1160	1165
Asn	Ala	Pro	Ser	Ile	Gly	Gln	Val	Asp	Ser	Ser	Lys	Gln	Phe	Glu	Gly		1170	1175	1180
Thr	Val	Glu	Ile	Lys	Arg	Lys	Phe	Ala	Gly	Leu	Leu	Lys	Asn	Asp	Cys		1185	1190	1195
Asn	Lys	Ser	Ala	Ser	Gly	Tyr	Leu	Thr	Asp	Glu	Asn	Glu	Val	Gly	Phe		1205	1210	1215
Arg	Gly	Phe	Tyr	Ser	Ala	His	Gly	Thr	Lys	Leu	Asn	Val	Ser	Thr	Glu		1220	1225	1230
Ala	Leu	Gln	Lys	Ala	Val	Lys	Leu	Phe	Ser	Asp	Ile	Glu	Asn	Ile	Ser				





Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly  
1700 1705 1710  
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp  
1715 1720 1725  
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser  
1730 1735 1740  
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser  
1745 1750 1755 1760  
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu  
1765 1770 1775  
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser  
1780 1785 1790  
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile  
1795 1800 1805  
Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn  
1810 1815 1820  
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly  
1825 1830 1835 1840  
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His  
1845 1850 1855  
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys  
1860 1865 1870  
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys  
1875 1880 1885  
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu  
1890 1895 1900  
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val  
1905 1910 1915 1920  
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met  
1925 1930 1935  
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu  
1940 1945 1950  
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser  
1955 1960 1965  
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys  
1970 1975 1980  
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe  
1985 1990 1995 2000  
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe  
2005 2010 2015  
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala  
2020 2025 2030  
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn  
2035 2040 2045  
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys  
2050 2055 2060  
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu  
2065 2070 2075 2080  
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro  
2085 2090 2095  
Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg  
2100 2105 2110  
Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys  
2115 2120 2125  
Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu  
2130 2135 2140  
Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln

2145		2150		2155		2160
Asp Lys Gln Gln Leu Val Leu Gly Thr		Lys Val Ser Leu Val Glu Asn				
	2165		2170		2175	
Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met						
	2180		2185		2190	
Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn						
	2195		2200		2205	
Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu						
	2210		2215		2220	
Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu						
2225	2230		2235		2240	
Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys						
	2245		2250		2255	
Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg						
	2260		2265		2270	
Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn						
	2275		2280		2285	
Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu						
	2290		2295		2300	
Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu						
2305	2310		2315		2320	
Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg						
	2325		2330		2335	
Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro						
	2340		2345		2350	
Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu						
	2355		2360		2365	
Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln						
	2370		2375		2380	
Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly						
2385	2390		2395		2400	
Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe						
	2405		2410		2415	
His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg						
	2420		2425		2430	
Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys						
	2435		2440		2445	
Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln						
	2450		2455		2460	
Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu						
2465	2470		2475		2480	
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys						
	2485		2490		2495	
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu						
	2500		2505		2510	
Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly						
	2515		2520		2525	
Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly						
	2530		2535		2540	
Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe						
2545	2550		2555		2560	
Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly						
	2565		2570		2575	
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp						
	2580		2585		2590	
Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro						
	2595		2600		2605	

Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr  
 2610 2615 2620  
 Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys  
 2625 2630 2635 2640  
 Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu  
 2645 2650 2655  
 Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile  
 2660 2665 2670  
 Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu  
 2675 2680 2685  
 Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser  
 2690 2695 2700  
 Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu  
 2705 2710 2715 2720  
 Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu  
 2725 2730 2735  
 Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile  
 2740 2745 2750  
 Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu  
 2755 2760 2765  
 Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg  
 2770 2775 2780  
 Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro  
 2785 2790 2795 2800  
 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly  
 2805 2810 2815  
 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu  
 2820 2825 2830  
 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu  
 2835 2840 2845  
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala  
 2850 2855 2860  
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr  
 2865 2870 2875 2880  
 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg  
 2885 2890 2895  
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala  
 2900 2905 2910  
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala  
 2915 2920 2925  
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile  
 2930 2935 2940  
 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln  
 2945 2950 2955 2960  
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser  
 2965 2970 2975  
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro  
 2980 2985 2990  
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile  
 2995 3000 3005  
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn  
 3010 3015 3020  
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val  
 3025 3030 3035 3040  
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His  
 3045 3050 3055  
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val

	3060		3065		3070										
Asp	Leu	Ile	Gly	Phe	Val	Val	Ser	Val	Val	Lys	Lys	Thr	Gly	Leu	Ala
	3075						3080					3085			
Pro	Phe	Val	Tyr	Leu	Ser	Asp	Glu	Cys	Tyr	Asn	Leu	Leu	Ala	Ile	Lys
	3090					3095					3100				
Phe	Trp	Ile	Asp	Leu	Asn	Glu	Asp	Ile	Ile	Lys	Pro	His	Met	Leu	Ile
3105				3110						3115				3120	
Ala	Ala	Ser	Asn	Leu	Gln	Trp	Arg	Pro	Glu	Ser	Lys	Ser	Gly	Leu	Leu
			3125						3130					3135	
Thr	Leu	Phe	Ala	Gly	Asp	Phe	Ser	Val	Phe	Ser	Ala	Ser	Pro	Lys	Glu
		3140					3145						3150		
Gly	His	Phe	Gln	Glu	Thr	Phe	Asn	Lys	Met	Lys	Asn	Thr	Val	Glu	Asn
	3155					3160						3165			
Ile	Asp	Ile	Leu	Cys	Asn	Glu	Ala	Glu	Asn	Lys	Leu	Met	His	Ile	Leu
	3170				3175						3180				
His	Ala	Asn	Asp	Pro	Lys	Trp	Ser	Thr	Pro	Thr	Lys	Asp	Cys	Thr	Ser
3185			3190							3195				3200	
Gly	Pro	Tyr	Thr	Ala	Gln	Ile	Ile	Pro	Gly	Thr	Gly	Asn	Lys	Leu	Leu
			3205						3210					3215	
Met	Ser	Ser	Pro	Asn	Cys	Glu	Ile	Tyr	Tyr	Gln	Ser	Pro	Leu	Ser	Leu
			3220					3225					3230		
Cys	Met	Ala	Lys	Arg	Lys	Ser	Val	Ser	Thr	Pro	Val	Ser	Ala	Gln	Met
	3235					3240					3245				
Thr	Ser	Lys	Ser	Cys	Lys	Gly	Glu	Lys	Glu	Ile	Asp	Asp	Gln	Lys	Asn
	3250				3255					3260					
Cys	Lys	Lys	Arg	Arg	Ala	Leu	Asp	Phe	Leu	Ser	Arg	Leu	Pro	Leu	Pro
3265			3270						3275					3280	
Pro	Pro	Val	Ser	Pro	Ile	Cys	Thr	Phe	Val	Ser	Pro	Ala	Ala	Gln	Lys
			3285						3290					3295	
Ala	Phe	Gln	Pro	Pro	Arg	Ser	Cys	Gly	Thr	Lys	Tyr	Glu	Thr	Pro	Ile
		3300					3305						3310		
Lys	Lys	Lys	Glu	Leu	Asn	Ser	Pro	Gln	Met	Thr	Pro	Phe	Lys	Lys	Phe
	3315					3320					3325				
Asn	Glu	Ile	Ser	Leu	Leu	Glu	Ser	Asn	Ser	Ile	Ala	Asp	Glu	Glu	Leu
	3330				3335					3340					
Ala	Leu	Ile	Asn	Thr	Gln	Ala	Leu	Leu	Ser	Gly	Ser	Thr	Gly	Glu	Lys
3345			3350						3355					3360	
Gln	Phe	Ile	Ser	Val	Ser	Glu	Ser	Thr	Arg	Thr	Ala	Pro	Thr	Ser	Ser
		3365						3370					3375		
Glu	Asp	Tyr	Leu	Arg	Leu	Lys	Arg	Arg	Cys	Thr	Thr	Ser	Leu	Ile	Lys
	3380				3385						3390				
Glu	Gln	Glu	Ser	Ser	Gln	Ala	Ser	Thr	Glu	Glu	Cys	Glu	Lys	Asn	Lys
	3395				3400						3405				
Gln	Asp	Thr	Ile	Thr	Thr	Lys	Lys	Tyr	Ile						
	3410				3415										

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10485 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 229...10482  
 (D) OTHER INFORMATION: BRCA2 (OMI3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC	60
TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTCGCC GCCGGGAGAA GCGTGAGGGG	120
ACAGATTTGT GACCGGCGCG GTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT	180
CTGGAGCGGA CTTATTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT	237
Met Pro Ile	
1	
GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC	285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys	
5 10 15	
AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT	333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu	
20 25 30 35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA	381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	
40 45 50	
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG	429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	
55 60 65	
AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG	477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	
70 75 80	
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT	525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	
85 90 95	
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA	573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	
100 105 110 115	
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC	621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser	
120 125 130	
TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	
135 140 145	
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
150 155 160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
165 170 175	

ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
180 185 190 195	
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	
200 205 210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	
215 220 225	
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
230 235 240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA	1005
Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg	
245 250 255	
GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA	1053
Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys	
260 265 270 275	
GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA CAT GTC CTA	1101
Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro His Val Leu	
280 285 290	
GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT	1149
Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser	
295 300 305	
TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA	1197
Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val	
310 315 320	
AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT	1245
Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp	
325 330 335	
GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA	1293
Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val	
340 345 350 355	
TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA	1341
Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala	
360 365 370	
AAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT	1389
Asn Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val	
375 380 385	
GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA	1437
Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu	
390 395 400	

AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT	1485
Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys	
405 410 415	
GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA	1533
Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg	
420 425 430 435	
AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC	1581
Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser	
440 445 450	
CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG	1629
Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys	
455 460 465	
AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA	1677
Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala	
470 475 480	
GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG	1725
Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln	
485 490 495	
GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT	1773
Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr	
500 505 510 515	
TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA	1821
Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys	
520 525 530	
GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA	1869
Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser	
535 540 545	
CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG	1917
Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp	
550 555 560	
CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA	1965
Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu	
565 570 575	
ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT	2013
Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His	
580 585 590 595	
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA	2061
Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser	
600 605 610	
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA	2109
Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala	
615 620 625	
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG	2157



Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His	Ser	Ser	Val	
		630					635					640				
AAA	AGA	AGC	TGT	TCA	CAG	AAT	GAT	TCT	GAA	GAA	CCA	ACT	TTG	TCC	TTA	2205
Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr	Leu	Ser	Leu	
		645				650					655					
ACT	AGC	TCT	TTT	GGG	ACA	ATT	CTG	AGG	AAA	TGT	TCT	AGA	AAT	GAA	ACA	2253
Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg	Asn	Glu	Thr	
		660			665					670				675		
TGT	TCT	AAT	AAT	ACA	GTA	ATC	TCT	CAG	GAT	CTT	GAT	TAT	AAA	GAA	GCA	2301
Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr	Lys	Glu	Ala	
				680					685					690		
AAA	TGT	AAT	AAG	GAA	AAA	CTA	CAG	TTA	TTT	ATT	ACC	CCA	GAA	GCT	GAT	2349
Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro	Glu	Ala	Asp	
			695				700						705			
TCT	CTG	TCA	TGC	CTG	CAG	GAA	GGA	CAG	TGT	GAA	AAT	GAT	CCA	AAA	AGC	2397
Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp	Pro	Lys	Ser	
		710					715					720				
AAA	AAA	GTT	TCA	GAT	ATA	AAA	GAA	GAG	GTC	TTG	GCT	GCA	GCA	TGT	CAC	2445
Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala	Ala	Cys	His	
		725				730					735					
CCA	GTA	CAA	CAC	TCA	AAA	GTG	GAA	TAC	AGT	GAT	ACT	GAC	TTT	CAA	TCC	2493
Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp	Phe	Gln	Ser	
					745				750					755		
CAG	AAA	AGT	CTT	TTA	TAT	GAT	CAT	GAA	AAT	GCC	AGC	ACT	CTT	ATT	TTA	2541
Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr	Leu	Ile	Leu	
			760						765					770		
ACT	CCT	ACT	TCC	AAG	GAT	GTT	CTG	TCA	AAC	CTA	GTC	ATG	ATT	TCT	AGA	2589
Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met	Ile	Ser	Arg	
			775				780						785			
GGC	AAA	GAA	TCA	TAC	AAA	ATG	TCA	GAC	AAG	CTC	AAA	GGT	AAC	AAT	TAT	2637
Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly	Asn	Asn	Tyr	
		790				795						800				
GAA	TCT	GAT	GTT	GAA	TTA	ACC	AAA	AAT	ATT	CCC	ATG	GAA	AAG	AAT	CAA	2685
Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu	Lys	Asn	Gln	
		805				810					815					
GAT	GTA	TGT	GCT	TTA	AAT	GAA	AAT	TAT	AAA	AAC	GTT	GAG	CTG	TTG	CCA	2733
Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu	Leu	Leu	Pro	
		820			825					830				835		
CCT	GAA	AAA	TAC	ATG	AGA	GTA	GCA	TCA	CCT	TCA	AGA	AAG	GTA	CAA	TTC	2781
Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys	Val	Gln	Phe	
			840						845					850		
AAC	CAA	AAC	ACA	AAT	CTA	AGA	GTA	ATC	CAA	AAA	AAT	CAA	GAA	GAA	ACT	2829
Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln	Glu	Glu	Thr	

855						860						865						
ACT	TCA	ATT	TCA	AAA	ATA	ACT	GTC	AAT	CCA	GAC	TCT	GAA	GAA	CTT	TTC	2877		
Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu	Glu	Leu	Phe			
		870					875					880						
TCA	GAC	AAT	GAG	AAT	AAT	TTT	GTC	TTC	CAA	GTA	GCT	AAT	GAA	AGG	AAT	2925		
Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Val	Ala	Asn	Glu	Arg	Asn			
	885					890					895							
AAT	CTT	GCT	TTA	GGA	AAT	ACT	AAG	GAA	CTT	CAT	GAA	ACA	GAC	TTG	ACT	2973		
Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu	Leu	His	Glu	Thr	Asp	Leu	Thr			
900					905					910				915				
TGT	GTA	AAC	GAA	CCC	ATT	TTC	AAG	AAC	TCT	ACC	ATG	GTT	TTA	TAT	GGA	3021		
Cys	Val	Asn	Glu	Pro	Ile	Phe	Lys	Asn	Ser	Thr	Met	Val	Leu	Tyr	Gly			
				920					925					930				
GAC	ACA	GGT	GAT	AAA	CAA	GCA	ACC	CAA	GTG	TCA	ATT	AAA	AAA	GAT	TTG	3069		
Asp	Thr	Gly	Asp	Lys	Gln	Ala	Thr	Gln	Val	Ser	Ile	Lys	Lys	Asp	Leu			
			935					940					945					
GTT	TAT	GTT	CTT	GCA	GAG	GAG	AAC	AAA	AAT	AGT	GTA	AAG	CAG	CAT	ATA	3117		
Val	Tyr	Val	Leu	Ala	Glu	Glu	Asn	Lys	Asn	Ser	Val	Lys	Gln	His	Ile			
		950					955					960						
AAA	ATG	ACT	CTA	GGT	CAA	GAT	TTA	AAA	TCG	GAC	ATC	TCC	TTG	AAT	ATA	3165		
Lys	Met	Thr	Leu	Gly	Gln	Asp	Leu	Lys	Ser	Asp	Ile	Ser	Leu	Asn	Ile			
	965					970					975							
GAT	AAA	ATA	CCA	GAA	AAA	AAT	AAT	GAT	TAC	ATG	GAC	AAA	TGG	GCA	GGA	3213		
Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asp	Lys	Trp	Ala	Gly			
980					985					990					995			
CTC	TTA	GGT	CCA	ATT	TCA	AAT	CAC	AGT	TTT	GGA	GGT	AGC	TTC	AGA	ACA	3261		
Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly	Gly	Ser	Phe	Arg	Thr			
			1000						1005				1010					
GCT	TCA	AAT	AAG	GAA	ATC	AAG	CTC	TCT	GAA	CAT	AAC	ATT	AAG	AAG	AGC	3309		
Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His	Asn	Ile	Lys	Lys	Ser			
		1015					1020					1025						
AAA	ATG	TTC	TTC	AAA	GAT	ATT	GAA	GAA	CAA	TAT	CCT	ACT	AGT	TTA	GCT	3357		
Lys	Met	Phe	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr	Pro	Thr	Ser	Leu	Ala			
	1030					1035					1040							
TGT	GTT	GAA	ATT	GTA	AAT	ACC	TTG	GCA	TTA	GAT	AAT	CAA	AAG	AAA	CTG	3405		
Cys	Val	Glu	Ile	Val	Asn	Thr	Leu	Ala	Leu	Asp	Asn	Gln	Lys	Lys	Leu			
	1045				1050					1055								
AGC	AAG	CCT	CAG	TCA	ATT	AAT	ACT	GTA	TCT	GCA	CAT	TTA	CAG	AGT	AGT	3453		
Ser	Lys	Pro	Gln	Ser	Ile	Asn	Thr	Val	Ser	Ala	His	Leu	Gln	Ser	Ser			
1060				1065				1070				1075						
GTA	GTT	GTT	TCT	GAT	TGT	AAA	AAT	AGT	CAT	ATA	ACC	CCT	CAG	ATG	TTA	3501		
Val	Val	Val	Ser	Asp	Cys	Lys	Asn	Ser	His	Ile	Thr	Pro	Gln	Met	Leu			
			1080				1085					1090						

TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA	3549
Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln	
1095 1100 1105	
AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT	3597
Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser	
1110 1115 1120	
CAG TTT GAA TTT ACT CAG TTT AGA AAG CCA AGC TAC ATA TTG CAG AAG	3645
Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys	
1125 1130 1135	
AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT	3693
Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr	
1140 1145 1150 1155	
TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA	3741
Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro	
1160 1165 1170	
TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA	3789
Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu	
1175 1180 1185	
ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT	3837
Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser	
1190 1195 1200	
GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT	3885
Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe	
1205 1210 1215	
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA	3933
Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln	
1220 1225 1230 1235	
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT	3981
Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr	
1240 1245 1250	
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT	4029
Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp	
1255 1260 1265	
TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA	4077
Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val	
1270 1275 1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA	4125
Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu	
1285 1290 1295	
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA	4173
Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg	
1300 1305 1310 1315	

AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser 1320 1325 1330	4221
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val 1335 1340 1345	4269
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn 1350 1355 1360	4317
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln 1365 1370 1375	4365
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala 1380 1385 1390 1395	4413
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala 1400 1405 1410	4461
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe 1415 1420 1425	4509
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe 1430 1435 1440	4557
AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn 1445 1450 1455	4605
TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met 1460 1465 1470 1475	4653
GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu 1480 1485 1490	4701
AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln 1495 1500 1505	4749
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly 1510 1515 1520	4797
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu 1525 1530 1535	4845
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA	4893

Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu	
1540 1545 1550 1555	
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG	4941
Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu	
1560 1565 1570	
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT	4989
Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala	
1575 1580 1585	
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC	5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn	
1590 1595 1600	
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT	5085
Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn	
1605 1610 1615	
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG	5133
Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu	
1620 1625 1630 1635	
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT	5181
Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro	
1640 1645 1650	
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA	5229
Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser	
1655 1660 1665	
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG	5277
Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln	
1670 1675 1680	
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT	5325
Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp	
1685 1690 1695	
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG	5373
Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu	
1700 1705 1710 1715	
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT	5421
Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His	
1720 1725 1730	
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC	5469
Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn	
1735 1740 1745	
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC	5517
Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu	
1750 1755 1760	
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT	5565
Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val	

1765	1770	1775	
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys 1780 1785 1790 1795			5613
GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu 1800 1805 1810			5661
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile 1815 1820 1825			5709
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala 1830 1835 1840			5757
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile 1845 1850 1855			5805
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys 1860 1865 1870 1875			5853
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala 1880 1885 1890			5901
GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser 1895 1900 1905			5949
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp 1910 1915 1920			5997
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu 1925 1930 1935			6045
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser 1940 1945 1950 1955			6093
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser 1960 1965 1970			6141
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln 1975 1980 1985			6189
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile 1990 1995 2000			6237

GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn 2005 2010 2015	6285
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr 2020 2025 2030 2035	6333
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn 2040 2045 2050	6381
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser 2055 2060 2065	6429
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe 2070 2075 2080	6477
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg 2085 2090 2095	6525
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu 2100 2105 2110 2115	6573
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys 2120 2125 2130	6621
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His 2135 2140 2145	6669
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln 2150 2155 2160	6717
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val 2165 2170 2175	6765
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly 2180 2185 2190 2195	6813
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val 2200 2205 2210	6861
TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala 2215 2220 2225	6909

GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser 2230 2235 2240	6957
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn 2245 2250 2255	7005
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu 2260 2265 2270 2275	7053
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn 2280 2285 2290	7101
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser 2295 2300 2305	7149
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His 2310 2315 2320	7197
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys 2325 2330 2335	7245
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu 2340 2345 2350 2355	7293
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser 2360 2365 2370	7341
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala 2375 2380 2385	7389
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr 2390 2395 2400	7437
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCG CAT TTT CAC AGA GTT Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val 2405 2410 2415	7485
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln 2420 2425 2430 2435	7533
AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp 2440 2445 2450	7581
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT	7629



Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala	
2455 2460 2465	
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT	7677
Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser	
2470 2475 2480	
CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA	7725
Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln	
2485 2490 2495	
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA	7773
Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr	
2500 2505 2510 2515	
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT	7821
Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val	
2520 2525 2530	
CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA	7869
Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys	
2535 2540 2545	
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC	7917
His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His	
2550 2555 2560	
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA	7965
Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile	
2565 2570 2575	
CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT	8013
Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala	
2580 2585 2590 2595	
GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT	8061
Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp	
2600 2605 2610	
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC	8109
Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile	
2615 2620 2625	
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT	8157
Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala	
2630 2635 2640	
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA	8205
Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg	
2645 2650 2655	
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA	8253
Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile	
2660 2665 2670 2675	
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT	8301
Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser	

2680	2685	2690	
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys 2695 2700 2705			8349
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp 2710 2715 2720			8397
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val 2725 2730 2735			8445
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly 2740 2745 2750 2755			8493
GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro 2760 2765 2770			8541
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg 2775 2780 2785			8589
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu 2790 2795 2800			8637
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp 2805 2810 2815			8685
GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser 2820 2825 2830 2835			8733
TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala 2840 2845 2850			8781
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr 2855 2860 2865			8829
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro 2870 2875 2880			8877
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln 2885 2890 2895			8925
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala 2900 2905 2910 2915			8973

TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT	9021
Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn	
2920 2925 2930	
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA	9069
His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu	
2935 2940 2945	
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA	9117
Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser	
2950 2955 2960	
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA	9165
Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys	
2965 2970 2975	
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT	9213
Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp	
2980 2985 2990 2995	
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT	9261
Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu	
3000 3005 3010	
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA	9309
Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu	
3015 3020 3025	
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA	9357
Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu	
3030 3035 3040	
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA	9405
Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys	
3045 3050 3055	
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA	9453
Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile	
3060 3065 3070 3075	
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC	9501
Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val	
3080 3085 3090	
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA	9549
Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile	
3095 3100 3105	
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC	9597
Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser	
3110 3115 3120	
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT	9645
Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe	
3125 3130 3135	

GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT	9693
Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe	
3140 3145 3150 3155	
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA	9741
Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile	
3160 3165 3170	
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT	9789
Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn	
3175 3180 3185	
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC	9837
Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr	
3190 3195 3200	
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT	9885
Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser	
3205 3210 3215	
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC	9933
Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala	
3220 3225 3230 3235	
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG	9981
Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys	
3240 3245 3250	
TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG	10029
Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys	
3255 3260 3265	
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT	10077
Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val	
3270 3275 3280	
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG	10125
Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln	
3285 3290 3295	
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA	10173
Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys	
3300 3305 3310 3315	
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT	10221
Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile	
3320 3325 3330	
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA	10269
Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile	
3335 3340 3345	
AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA	10317
Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile	
3350 3355 3360	
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT	10365

Ser Val	Ser Glu	Ser Thr	Arg Thr	Ala Pro	Thr Ser	Ser Ser	Glu Asp	Tyr	
3365			3370		3375				
CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG	10413								
Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu									
3380		3385		3390		3395			
AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA	10461								
Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr									
	3400		3405		3410				
ATT ACA ACT AAA AAA TAT ATC TAA	10485								
Ile Thr Thr Lys Lys Tyr Ile									
	3415								

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Pro	Ile	Gly	Ser	Lys	Glu	Arg	Pro	Thr	Phe	Phe	Glu	Ile	Phe	Lys
1				5					10					15	
Thr	Arg	Cys	Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe
			20					25					30		
Glu	Glu	Leu	Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu
		35					40					45			
Glu	Ser	Glu	His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr
	50				55					60					
Pro	Gln	Arg	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile
65				70				75						80	
Phe	Lys	Glu	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys
			85					90						95	
Glu	Leu	Asp	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser
		100						105					110		
Arg	His	Lys	Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp
	115						120					125			
Asp	Val	Ser	Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val
	130					135					140				
Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val
145					150					155					160
Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr
			165					170						175	
Pro	Lys	His	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met
		180						185					190		
Ser	Trp	Ser	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val
	195					200						205			
Leu	Ile	Val	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp
	210					215									

Thr	Thr	Ala	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu
225					230					235					240
Lys	Lys	Asn	Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr
				245					250					255	
Asn	Gln	Arg	Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn
			260					265					270		
Ser	Phe	Lys	Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro
		275					280					285			
His	Val	Leu	Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu
	290					295					300				
Glu	Asp	Ser	Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu
305					310					315					320
Gln	Lys	Val	Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala
				325					330					335	
Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr
		340						345					350		
Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser
		355					360					365			
Asn	Val	Ala	Asn	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser
	370					375					380				
Lys	Glu	Val	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu
385					390					395					400
Ser	Gly	Leu	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile
				405					410					415	
Ser	Ser	Cys	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu
			420					425					430		
Asn	Lys	Arg	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg
		435					440					445			
Ile	Ser	Ser	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val
	450					455					460				
Val	Asn	Lys	Arg	Asp	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys	
465					470				475					480	
Ile	Leu	Ala	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser
				485					490					495	
Ser	Phe	Gln	Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro
		500						505					510		
Lys	Glu	Thr	Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn
		515					520					525			
Phe	Lys	Lys	Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr
	530					535					540				
Val	Cys	Ser	Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn
545					550					555					560
Gly	Ser	Trp	Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn
				565					570					575	
Ala	Gly	Leu	Ile	Ser	Thr	Leu	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr	
		580						585				590			
Ala	Ile	His	Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp
		595					600					605			
Gln	Lys	Ser	Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala
	610					615					620				
Phe	Glu	Ala	Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His
625					630					635					640
Ser	Ser	Val	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr
				645					650					655	
Leu	Ser	Leu	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg
			660					665					670		
Asn	Glu	Thr	Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr



Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu  
 1140 1145 1150  
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met  
 1155 1160 1165  
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly  
 1170 1175 1180  
 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys  
 1185 1190 1195 1200  
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe  
 1205 1210 1215  
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu  
 1220 1225 1230  
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser  
 1235 1240 1245  
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys  
 1250 1255 1260  
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp  
 1265 1270 1275 1280  
 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn  
 1285 1290 1295  
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn  
 1300 1305 1310  
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser  
 1315 1320 1325  
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn  
 1330 1335 1340  
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp  
 1345 1350 1355 1360  
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly  
 1365 1370 1375  
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val  
 1380 1385 1390  
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln  
 1395 1400 1405  
 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser  
 1410 1415 1420  
 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys  
 1425 1430 1435 1440  
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu  
 1445 1450 1455  
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys  
 1460 1465 1470  
 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His  
 1475 1480 1485  
 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val  
 1490 1495 1500  
 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr  
 1505 1510 1515 1520  
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys  
 1525 1530 1535  
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly  
 1540 1545 1550  
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys  
 1555 1560 1565  
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu  
 1570 1575 1580  
 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn



1585		1590		1595		1600
Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu						
	1605			1610		1615
Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser						
	1620			1625		1630
Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala						
	1635			1640		1645
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile						
	1650			1655		1660
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser						
1665		1670		1675		1680
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly						
	1685			1690		1695
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly						
	1700			1705		1710
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp						
	1715			1720		1725
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser						
	1730			1735		1740
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser						
1745		1750		1755		1760
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu						
	1765			1770		1775
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser						
	1780			1785		1790
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile						
	1795			1800		1805
Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn						
	1810			1815		1820
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly						
1825		1830		1835		1840
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His						
	1845			1850		1855
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys						
	1860			1865		1870
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys						
	1875			1880		1885
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu						
	1890			1895		1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val						
1905		1910		1915		1920
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met						
	1925			1930		1935
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu						
	1940			1945		1950
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser						
	1955			1960		1965
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys						
	1970			1975		1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe						
1985		1990		1995		2000
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe						
	2005			2010		2015
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala						
	2020			2025		2030
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn						
	2035			2040		2045



			2500				2505				2510				
Ala	Lys	Thr	Ser	Thr	Leu	Pro	Arg	Ile	Ser	Leu	Lys	Ala	Ala	Val	Gly
			2515				2520				2525				
Gly	Gln	Val	Pro	Ser	Ala	Cys	Ser	His	Lys	Gln	Leu	Tyr	Thr	Tyr	Gly
			2530				2535				2540				
Val	Ser	Lys	His	Cys	Ile	Lys	Ile	Asn	Ser	Lys	Asn	Ala	Glu	Ser	Phe
2545			2550				2555				2560				
Gln	Phe	His	Thr	Glu	Asp	Tyr	Phe	Gly	Lys	Glu	Ser	Leu	Trp	Thr	Gly
			2565				2570				2575				
Lys	Gly	Ile	Gln	Leu	Ala	Asp	Gly	Gly	Trp	Leu	Ile	Pro	Ser	Asn	Asp
			2580				2585				2590				
Gly	Lys	Ala	Gly	Lys	Glu	Glu	Phe	Tyr	Arg	Ala	Leu	Cys	Asp	Thr	Pro
			2595				2600				2605				
Gly	Val	Asp	Pro	Lys	Leu	Ile	Ser	Arg	Ile	Trp	Val	Tyr	Asn	His	Tyr
			2610				2615				2620				
Arg	Trp	Ile	Ile	Trp	Lys	Leu	Ala	Ala	Met	Glu	Cys	Ala	Phe	Pro	Lys
2625			2630				2635				2640				
Glu	Phe	Ala	Asn	Arg	Cys	Leu	Ser	Pro	Glu	Arg	Val	Leu	Leu	Gln	Leu
			2645				2650				2655				
Lys	Tyr	Arg	Tyr	Asp	Thr	Glu	Ile	Asp	Arg	Ser	Arg	Arg	Ser	Ala	Ile
			2660				2665				2670				
Lys	Lys	Ile	Met	Glu	Arg	Asp	Asp	Thr	Ala	Ala	Lys	Thr	Leu	Val	Leu
			2675				2680				2685				
Cys	Val	Ser	Asp	Ile	Ile	Ser	Leu	Ser	Ala	Asn	Ile	Ser	Glu	Thr	Ser
2690			2695				2700								
Ser	Asn	Lys	Thr	Ser	Ser	Ala	Asp	Thr	Gln	Lys	Val	Ala	Ile	Ile	Glu
2705			2710				2715				2720				
Leu	Thr	Asp	Gly	Trp	Tyr	Ala	Val	Lys	Ala	Gln	Leu	Asp	Pro	Pro	Leu
			2725				2730				2735				
Leu	Ala	Val	Leu	Lys	Asn	Gly	Arg	Leu	Thr	Val	Gly	Gln	Lys	Ile	Ile
			2740				2745				2750				
Leu	His	Gly	Ala	Glu	Leu	Val	Gly	Ser	Pro	Asp	Ala	Cys	Thr	Pro	Leu
			2755				2760				2765				
Glu	Ala	Pro	Glu	Ser	Leu	Met	Leu	Lys	Ile	Ser	Ala	Asn	Ser	Thr	Arg
			2770				2775				2780				
Pro	Ala	Arg	Trp	Tyr	Thr	Lys	Leu	Gly	Phe	Phe	Pro	Asp	Pro	Arg	Pro
2785			2790				2795				2800				
Phe	Pro	Leu	Pro	Leu	Ser	Ser	Leu	Phe	Ser	Asp	Gly	Gly	Asn	Val	Gly
			2805				2810				2815				
Cys	Val	Asp	Val	Ile	Ile	Gln	Arg	Ala	Tyr	Pro	Ile	Gln	Trp	Met	Glu
			2820				2825				2830				
Lys	Thr	Ser	Ser	Gly	Leu	Tyr	Ile	Phe	Arg	Asn	Glu	Arg	Glu	Glu	Glu
			2835				2840				2845				
Lys	Glu	Ala	Ala	Lys	Tyr	Val	Glu	Ala	Gln	Gln	Lys	Arg	Leu	Glu	Ala
			2850				2855				2860				
Leu	Phe	Thr	Lys	Ile	Gln	Glu	Glu	Phe	Glu	Glu	His	Glu	Glu	Asn	Thr
2865			2870				2875				2880				
Thr	Lys	Pro	Tyr	Leu	Pro	Ser	Arg	Ala	Leu	Thr	Arg	Gln	Gln	Val	Arg
			2885				2890				2895				
Ala	Leu	Gln	Asp	Gly	Ala	Glu	Leu	Tyr	Glu	Ala	Val	Lys	Asn	Ala	Ala
			2900				2905				2910				
Asp	Pro	Ala	Tyr	Leu	Glu	Gly	Tyr	Phe	Ser	Glu	Glu	Gln	Leu	Arg	Ala
			2915				2920				2925				
Leu	Asn	Asn	His	Arg	Gln	Met	Leu	Asn	Asp	Lys	Lys				



3410

3415

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI4)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC      60
TCTGCTGCGC CTCGGGTGTC TTTTGC GGCG GTGGGTCGCC GCCGGGAGAA GCGTGAGGGG      120
ACAGATTTGT GACCGGCGCG GTTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT      180
CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT      237
                                     Met Pro Ile
                                     1

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC      285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
      5                      10                      15

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT      333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu
20                      25                      30                      35

TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA      381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu
      40                      45                      50

CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG      429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg
      55                      60                      65

AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG      477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu
      70                      75                      80

CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT      525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp
      85                      90                      95

AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA      573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys
100                      105                      110                      115

AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC      621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser

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	120	125	130	
TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA				669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln				
	135	140	145	
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT				717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser				
	150	155	160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT				765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His				
	165	170	175	
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA				813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser				
	180	185	190	195
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC				861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val				
	200	205	210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT				909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala				
	215	220	225	
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT				957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn				
	230	235	240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA				1005
Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg				
	245	250	255	
GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA				1053
Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys				
	260	265	270	275
GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA AAT GTC CTA				1101
Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu				
	280	285	290	
GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT				1149
Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser				
	295	300	305	
TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA				1197
Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val				
	310	315	320	
AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT				1245
Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp				
	325	330	335	
GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA				1293
Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val				
	340	345	350	355

TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA	1341
Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala	
360 365 370	
CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT	1389
His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val	
375 380 385	
GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA	1437
Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu	
390 395 400	
AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT	1485
Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys	
405 410 415	
GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA	1533
Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg	
420 425 430 435	
AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC	1581
Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser	
440 445 450	
CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG	1629
Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys	
455 460 465	
AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA	1677
Arg Asp Glu Glu Gln His Leu Ser His Thr Asp Cys Ile Leu Ala	
470 475 480	
GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG	1725
Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln	
485 490 495	
GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT	1773
Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr	
500 505 510 515	
TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA	1821
Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys	
520 525 530	
GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA	1869
Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser	
535 540 545	
CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG	1917
Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp	
550 555 560	
CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA	1965
Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu	
565 570 575	

ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT	2013
Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His	
580 585 590 595	
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA	2061
Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser	
600 605 610	
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA	2109
Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala	
615 620 625	
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG	2157
Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val	
630 635 640	
AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA	2205
Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu	
645 650 655	
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA	2253
Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr	
660 665 670 675	
TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA	2301
Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala	
680 685 690	
AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT	2349
Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp	
695 700 705	
TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC	2397
Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser	
710 715 720	
AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC	2445
Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His	
725 730 735	
CCA GTA CAA CAT TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC	2493
Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser	
740 745 750 755	
CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA	2541
Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu	
760 765 770	
ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA	2589
Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg	
775 780 785	
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT	2637
Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr	
790 795 800	
GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA	2685



Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu	Lys	Asn	Gln	
805						810					815					
GAT	GTA	TGT	GCT	TTA	AAT	GAA	AAT	TAT	AAA	AAC	GTT	GAG	CTG	TTG	CCA	2733
Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu	Leu	Leu	Pro	
820					825				830						835	
CCT	GAA	AAA	TAC	ATG	AGA	GTA	GCA	TCA	CCT	TCA	AGA	AAG	GTA	CAA	TTC	2781
Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys	Val	Gln	Phe	
				840					845					850		
AAC	CAA	AAC	ACA	AAT	CTA	AGA	GTA	ATC	CAA	AAA	AAT	CAA	GAA	GAA	ACT	2829
Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln	Glu	Glu	Thr	
			855					860					865			
ACT	TCA	ATT	TCA	AAA	ATA	ACT	GTC	AAT	CCA	GAC	TCT	GAA	GAA	CTT	TTC	2877
Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu	Glu	Leu	Phe	
		870					875					880				
TCA	GAC	AAT	GAG	AAT	AAT	TTT	GTC	TTC	CAA	GTA	GCT	AAT	GAA	AGG	AAT	2925
Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Val	Ala	Asn	Glu	Arg	Asn	
	885					890					895					
AAT	CTT	GCT	TTA	GGA	AAT	ACT	AAG	GAA	CTT	CAT	GAA	ACA	GAC	TTG	ACT	2973
Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu	Leu	His	Glu	Thr	Asp	Leu	Thr	
900					905					910					915	
TGT	GTA	AAC	GAA	CCC	ATT	TTC	AAG	AAC	TCT	ACC	ATG	GTT	TTA	TAT	GGA	3021
Cys	Val	Asn	Glu	Pro	Ile	Phe	Lys	Asn	Ser	Thr	Met	Val	Leu	Tyr	Gly	
				920					925					930		
GAC	ACA	GGT	GAT	AAA	CAA	GCA	ACC	CAA	GTG	TCA	ATT	AAA	AAA	GAT	TTG	3069
Asp	Thr	Gly	Asp	Lys	Gln	Ala	Thr	Gln	Val	Ser	Ile	Lys	Lys	Asp	Leu	
			935					940					945			
GTT	TAT	GTT	CTT	GCA	GAG	GAG	AAC	AAA	AAT	AGT	GTA	AAG	CAG	CAT	ATA	3117
Val	Tyr	Val	Leu	Ala	Glu	Glu	Asn	Lys	Asn	Ser	Val	Lys	Gln	His	Ile	
		950					955					960				
AAA	ATG	ACT	CTA	GGT	CAA	GAT	TTA	AAA	TCG	GAC	ATC	TCC	TTG	AAT	ATA	3165
Lys	Met	Thr	Leu	Gly	Gln	Asp	Leu	Lys	Ser	Asp	Ile	Ser	Leu	Asn	Ile	
	965					970					975					
GAT	AAA	ATA	CCA	GAA	AAA	AAT	AAT	GAT	TAC	ATG	AAC	AAA	TGG	GCA	GGA	3213
Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asn	Lys	Trp	Ala	Gly	
980					985				990						995	
CTC	TTA	GGT	CCA	ATT	TCA	AAT	CAC	AGT	TTT	GGA	GGT	AGC	TTC	AGA	ACA	3261
Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly	Gly	Ser	Phe	Arg	Thr	
			1000						1005					1010		
GCT	TCA	AAT	AAG	GAA	ATC	AAG	CTC	TCT	GAA	CAT	AAC	ATT	AAG	AAG	AGC	3309
Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His	Asn	Ile	Lys	Lys	Ser	
			1015				1020					1025				
AAA	ATG	TTC	TTC	AAA	GAT	ATT	GAA	GAA	CAA	TAT	CCT	ACT	AGT	TTA	GCT	3357
Lys	Met	Phe	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr	Pro	Thr	Ser	Leu	Ala	

1030	1035	1040	
TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu 1045 1050 1055			3405
AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser 1060 1065 1070 1075			3453
GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu 1080 1085 1090			3501
TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln 1095 1100 1105			3549
AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser 1110 1115 1120			3597
CAG TTT GAA TTT ACT CAG TTT AGA AAG CCA AGC TAC ATA TTG CAG AAG Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys 1125 1130 1135			3645
AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr 1140 1145 1150 1155			3693
TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro 1160 1165 1170			3741
TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu 1175 1180 1185			3789
ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser 1190 1195 1200			3837
GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe 1205 1210 1215			3885
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln 1220 1225 1230 1235			3933
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr 1240 1245 1250			3981
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp 1255 1260 1265			4029

TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA	4077
Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val	
1270 1275 1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA	4125
Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu	
1285 1290 1295	
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA	4173
Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg	
1300 1305 1310 1315	
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT	4221
Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser	
1320 1325 1330	
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT	4269
His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val	
1335 1340 1345	
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC	4317
Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn	
1350 1355 1360	
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG	4365
Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln	
1365 1370 1375	
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT	4413
Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala	
1380 1385 1390 1395	
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT	4461
Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala	
1400 1405 1410	
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT	4509
Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe	
1415 1420 1425	
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT	4557
Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe	
1430 1435 1440	
AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC	4605
Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn	
1445 1450 1455	
TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG	4653
Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met	
1460 1465 1470 1475	
GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG	4701
Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu	
1480 1485 1490	

AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln 1495 1500 1505	4749
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly 1510 1515 1520	4797
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu 1525 1530 1535	4845
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu 1540 1545 1550 1555	4893
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu 1560 1565 1570	4941
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala 1575 1580 1585	4989
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn 1590 1595 1600	5037
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn 1605 1610 1615	5085
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu 1620 1625 1630 1635	5133
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro 1640 1645 1650	5181
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser 1655 1660 1665	5229
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln 1670 1675 1680	5277
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp 1685 1690 1695	5325
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu 1700 1705 1710 1715	5373
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT	5421

Tyr	Glu	Asn	Asn	Ser	Asn	Ser	Thr	Ile	Ala	Glu	Asn	Asp	Lys	Asn	His	
				1720					1725					1730		
CTC	TCC	GAA	AAA	CAA	GAT	ACT	TAT	TTA	AGT	AAC	AGT	AGC	ATG	TCT	AAC	5469
Leu	Ser	Glu	Lys	Gln	Asp	Thr	Tyr	Leu	Ser	Asn	Ser	Ser	Met	Ser	Asn	
			1735					1740					1745			
AGC	TAT	TCC	TAC	CAT	TCT	GAT	GAG	GTA	TAT	AAT	GAT	TCA	GGA	TAT	CTC	5517
Ser	Tyr	Ser	Tyr	His	Ser	Asp	Glu	Val	Tyr	Asn	Asp	Ser	Gly	Tyr	Leu	
		1750					1755					1760				
TCA	AAA	AAT	AAA	CTT	GAT	TCT	GGT	ATT	GAG	CCA	GTA	TTG	AAG	AAT	GTT	5565
Ser	Lys	Asn	Lys	Leu	Asp	Ser	Gly	Ile	Glu	Pro	Val	Leu	Lys	Asn	Val	
	1765					1770				1775						
GAA	GAT	CAA	AAA	AAC	ACT	AGT	TTT	TCC	AAA	GTA	ATA	TCC	AAT	GTA	AAA	5613
Glu	Asp	Gln	Lys	Asn	Thr	Ser	Phe	Ser	Lys	Val	Ile	Ser	Asn	Val	Lys	
1780				1785					1790					1795		
GAT	GCA	AAT	GCA	TAC	CCA	CAA	ACT	GTA	AAT	GAA	GAT	ATT	TGC	GTT	GAG	5661
Asp	Ala	Asn	Ala	Tyr	Pro	Gln	Thr	Val	Asn	Glu	Asp	Ile	Cys	Val	Glu	
			1800					1805					1810			
GAA	CTT	GTG	ACT	AGC	TCT	TCA	CCC	TGC	AAA	AAT	AAA	AAT	GCA	GCC	ATT	5709
Glu	Leu	Val	Thr	Ser	Ser	Ser	Pro	Cys	Lys	Asn	Lys	Asn	Ala	Ala	Ile	
		1815					1820					1825				
AAA	TTG	TCC	ATA	TCT	AAT	AGT	AAT	AAT	TTT	GAG	GTA	GGG	CCA	CCT	GCA	5757
Lys	Leu	Ser	Ile	Ser	Asn	Ser	Asn	Asn	Phe	Glu	Val	Gly	Pro	Pro	Ala	
	1830					1835				1840						
TTT	AGG	ATA	GCC	AGT	GGT	AAA	ATC	GTT	TGT	GTT	TCA	CAT	GAA	ACA	ATT	5805
Phe	Arg	Ile	Ala	Ser	Gly	Lys	Ile	Val	Cys	Val	Ser	His	Glu	Thr	Ile	
	1845				1850				1855							
AAA	AAA	GTG	AAA	GAC	ATA	TTT	ACA	GAC	AGT	TTC	AGT	AAA	GTA	ATT	AAG	5853
Lys	Lys	Val	Lys	Asp	Ile	Phe	Thr	Asp	Ser	Phe	Ser	Lys	Val	Ile	Lys	
1860				1865				1870				1875				
GAA	AAC	AAC	GAG	AAT	AAA	TCA	AAA	ATT	TGC	CAA	ACG	AAA	ATT	ATG	GCA	5901
Glu	Asn	Asn	Glu	Asn	Lys	Ser	Lys	Ile	Cys	Gln	Thr	Lys	Ile	Met	Ala	
			1880					1885				1890				
GGT	TGT	TAC	GAG	GCA	TTG	GAT	GAT	TCA	GAG	GAT	ATT	CTT	CAT	AAC	TCT	5949
Gly	Cys	Tyr	Glu	Ala	Leu	Asp	Asp	Ser	Glu	Asp	Ile	Leu	His	Asn	Ser	
		1895					1900					1905				
CTA	GAT	AAT	GAT	GAA	TGT	AGC	ACG	CAT	TCA	CAT	AAG	GTT	TTT	GCT	GAC	5997
Leu	Asp	Asn	Asp	Glu	Cys	Ser	Thr	His	Ser	His	Lys	Val	Phe	Ala	Asp	
	1910						1915					1920				
ATT	CAG	AGT	GAA	GAA	ATT	TTA	CAA	CAT	AAC	CAA	AAT	ATG	TCT	GGA	TTG	6045
Ile	Gln	Ser	Glu	Glu	Ile	Leu	Gln	His	Asn	Gln	Asn	Met	Ser	Gly	Leu	
	1925					1930				1935						
GAG	AAA	GTT	TCT	AAA	ATA	TCA	CCT	TGT	GAT	GTT	AGT	TTG	GAA	ACT	TCA	6093
Glu	Lys	Val	Ser	Lys	Ile	Ser	Pro	Cys	Asp	Val	Ser	Leu	Glu	Thr	Ser	

1940						1945						1950						1955	
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser	1960					1965					1970					6141			
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln	1975					1980					1985					6189			
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile	1990					1995					2000					6237			
GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn	2005					2010					2015					6285			
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr	2020					2025					2030					2035		6333	
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn	2040					2045					2050					6381			
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser	2055					2060					2065					6429			
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe	2070					2075					2080					6477			
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg	2085					2090					2095					6525			
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu	2100					2105					2110					2115		6573	
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys	2120					2125					2130					6621			
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His	2135					2140					2145					6669			
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln	2150					2155					2160					6717			
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val	2165					2170					2175					6765			

TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT	6813
Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly	
2180 2185 2190 2195	
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT	6861
Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val	
2200 2205 2210	
TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA	6909
Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala	
2215 2220 2225	
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT	6957
Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser	
2230 2235 2240	
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT	7005
Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn	
2245 2250 2255	
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG	7053
Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu	
2260 2265 2270 2275	
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT	7101
Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn	
2280 2285 2290	
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA	7149
Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser	
2295 2300 2305	
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT	7197
Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His	
2310 2315 2320	
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG	7245
His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys	
2325 2330 2335	
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA	7293
Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu	
2340 2345 2350 2355	
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT	7341
Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser	
2360 2365 2370	
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT	7389
Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala	
2375 2380 2385	
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC	7437
Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr	
2390 2395 2400	

AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCG CAT TTT CAC AGA GTT Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val 2405 2410 2415	7485
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln 2420 2425 2430 2435	7533
AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp 2440 2445 2450	7581
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala 2455 2460 2465	7629
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser 2470 2475 2480	7677
CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln 2485 2490 2495	7725
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr 2500 2505 2510 2515	7773
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val 2520 2525 2530	7821
CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys 2535 2540 2545	7869
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His 2550 2555 2560	7917
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile 2565 2570 2575	7965
CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala 2580 2585 2590 2595	8013
GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp 2600 2605 2610	8061
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile 2615 2620 2625	8109
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT	8157



Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala	
2630 2635 2640	
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA	8205
Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg	
2645 2650 2655	
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA	8253
Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile	
2660 2665 2670 2675	
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT	8301
Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser	
2680 2685 2690	
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA	8349
Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys	
2695 2700 2705	
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT	8397
Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp	
2710 2715 2720	
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC	8445
Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val	
2725 2730 2735	
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA	8493
Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly	
2740 2745 2750 2755	
GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA	8541
Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro	
2760 2765 2770	
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC	8589
Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg	
2775 2780 2785	
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG	8637
Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu	
2790 2795 2800	
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT	8685
Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp	
2805 2810 2815	
GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA	8733
Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser	
2820 2825 2830 2835	
TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA	8781
Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala	
2840 2845 2850	
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT	8829
Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr	

2855	2860	2865	
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro 2870 2875 2880			8877
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln 2885 2890 2895			8925
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala 2900 2905 2910 2915			8973
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn 2920 2925 2930			9021
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu 2935 2940 2945			9069
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser 2950 2955 2960			9117
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys 2965 2970 2975			9165
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp 2980 2985 2990 2995			9213
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu 3000 3005 3010			9261
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu 3015 3020 3025			9309
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu 3030 3035 3040			9357
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys 3045 3050 3055			9405
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile 3060 3065 3070 3075			9453
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val 3080 3085 3090			9501

TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA	9549
Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile	
3095 3100 3105	
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC	9597
Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser	
3110 3115 3120	
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT	9645
Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe	
3125 3130 3135	
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT	9693
Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe	
3140 3145 3150 3155	
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA	9741
Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile	
3160 3165 3170	
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT	9789
Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn	
3175 3180 3185	
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC	9837
Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr	
3190 3195 3200	
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT	9885
Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser	
3205 3210 3215	
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC	9933
Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala	
3220 3225 3230 3235	
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG	9981
Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys	
3240 3245 3250	
TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG	10029
Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys	
3255 3260 3265	
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT	10077
Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Val	
3270 3275 3280	
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG	10125
Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln	
3285 3290 3295	
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA	10173
Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys	
3300 3305 3310 3315	

GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT	10221
Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile	
3320 3325 3330	
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA	10269
Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile	
3335 3340 3345	
AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA	10317
Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile	
3350 3355 3360	
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT	10365
Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr	
3365 3370 3375	
CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG	10413
Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu	
3380 3385 3390 3395	
AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA	10461
Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr	
3400 3405 3410	
ATT ACA ACT AAA AAA TAT ATC TAA	10485
Ile Thr Thr Lys Lys Tyr Ile	
3415	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys	
1 5 10 15	
Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe	
20 25 30	
Glu Glu Leu Ser Ser Glu Ala Pro Tyr Asn Ser Glu Pro Ala Glu	
35 40 45	
Glu Ser Glu His Lys Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr	
50 55 60	
Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile	
65 70 75 80	
Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys	
85 90 95	
Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser	
100 105 110	
Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp	



Ala	Gly	Leu	Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr	580	585	590
Ala	Ile	His	Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp	595	600	605
Gln	Lys	Ser	Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala	610	615	620
Phe	Glu	Ala	Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His	625	630	635
Ser	Ser	Val	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr	645	650	655
Leu	Ser	Leu	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg	660	665	670
Asn	Glu	Thr	Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr	675	680	685
Lys	Glu	Ala	Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro	690	695	700
Glu	Ala	Asp	Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp	705	710	715
Pro	Lys	Ser	Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala	725	730	735
Ala	Cys	His	Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp	740	745	750
Phe	Gln	Ser	Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr	755	760	765
Leu	Ile	Leu	Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met	770	775	780
Ile	Ser	Arg	Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly	785	790	795
Asn	Asn	Tyr	Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu	805	810	815
Lys	Asn	Gln	Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu	820	825	830
Leu	Leu	Pro	Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys	835	840	845
Val	Gln	Phe	Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln	850	855	860
Glu	Glu	Thr	Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu	865	870	875
Glu	Leu	Phe	Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Val	Ala	Asn	885	890	895
Glu	Arg	Asn	Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu	Leu	His	Glu	Thr	900	905	910
Asp	Leu	Thr	Cys	Val	Asn	Glu	Pro	Ile	Phe	Lys	Asn	Ser	Thr	Met	Val	915	920	925
Leu	Tyr	Gly	Asp	Thr	Gly	Asp	Lys	Gln	Ala	Thr	Gln	Val	Ser	Ile	Lys	930	935	940
Lys	Asp	Leu	Val	Tyr	Val	Leu	Ala	Glu	Glu	Asn	Lys	Asn	Ser	Val	Lys	945	950	955
Gln	His	Ile	Lys	Met	Thr	Leu	Gly	Gln	Asp	Leu	Lys	Ser	Asp	Ile	Ser	965	970	975
Leu	Asn	Ile	Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asn	Lys	980	985	990
Trp	Ala	Gly	Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly	Gly	Ser	995	1000	1005
Phe	Arg	Thr	Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His	Asn	Ile	1010	1015	1020
Lys	Lys	Ser	Lys	Met	Phe	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr	Pro	Thr			

1025		1030		1035		1040
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln						
	1045		1050		1055	
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu						
	1060		1065		1070	
Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro						
	1075		1080		1085	
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr						
	1090		1095		1100	
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu						
1105		1110		1115		1120
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile						
	1125		1130		1135	
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu						
	1140		1145		1150	
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met						
	1155		1160		1165	
Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly						
	1170		1175		1180	
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys						
1185		1190		1195		1200
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe						
	1205		1210		1215	
Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu						
	1220		1225		1230	
Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser						
	1235		1240		1245	
Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys						
	1250		1255		1260	
Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp						
1265		1270		1275		1280
Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn						
	1285		1290		1295	
Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn						
	1300		1305		1310	
Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser						
	1315		1320		1325	
Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn						
	1330		1335		1340	
Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp						
1345		1350		1355		1360
Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly						
	1365		1370		1375	
Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val						
	1380		1385		1390	
Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln						
	1395		1400		1405	
Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser						
	1410		1415		1420	
Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys						
1425		1430		1435		1440
Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu						
	1445		1450		1455	
Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys						
	1460		1465		1470	
Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His						
	1475		1480		1485	

Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val  
 1490 1495 1500  
 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr  
 1505 1510 1515 1520  
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys  
 1525 1530 1535  
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly  
 1540 1545 1550  
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys  
 1555 1560 1565  
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu  
 1570 1575 1580  
 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn  
 1585 1590 1595 1600  
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu  
 1605 1610 1615  
 Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser  
 1620 1625 1630  
 Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala  
 1635 1640 1645  
 Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile  
 1650 1655 1660  
 Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser  
 1665 1670 1675 1680  
 Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly  
 1685 1690 1695  
 Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly  
 1700 1705 1710  
 Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp  
 1715 1720 1725  
 Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser  
 1730 1735 1740  
 Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser  
 1745 1750 1755 1760  
 Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu  
 1765 1770 1775  
 Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser  
 1780 1785 1790  
 Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile  
 1795 1800 1805  
 Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn  
 1810 1815 1820  
 Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly  
 1825 1830 1835 1840  
 Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His  
 1845 1850 1855  
 Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys  
 1860 1865 1870  
 Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys  
 1875 1880 1885  
 Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu  
 1890 1895 1900  
 His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val  
 1905 1910 1915 1920  
 Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met  
 1925 1930 1935  
 Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu



				1940						1945					1950		
Glu	Thr	Ser	Asp	Ile	Cys	Lys	Cys	Ser	Ile	Gly	Lys	Leu	His	Lys	Ser		
		1955					1960					1965					
Val	Ser	Ser	Ala	Asn	Thr	Cys	Gly	Ile	Phe	Ser	Thr	Ala	Ser	Gly	Lys		
	1970					1975					1980						
Ser	Val	Gln	Val	Ser	Asp	Ala	Ser	Leu	Gln	Asn	Ala	Arg	Gln	Val	Phe		
1985					1990					1995					2000		
Ser	Glu	Ile	Glu	Asp	Ser	Thr	Lys	Gln	Val	Phe	Ser	Lys	Val	Leu	Phe		
				2005				2010						2015			
Lys	Ser	Asn	Glu	His	Ser	Asp	Gln	Leu	Thr	Arg	Glu	Glu	Asn	Thr	Ala		
			2020					2025					2030				
Ile	Arg	Thr	Pro	Glu	His	Leu	Ile	Ser	Gln	Lys	Gly	Phe	Ser	Tyr	Asn		
		2035					2040					2045					
Val	Val	Asn	Ser	Ser	Ala	Phe	Ser	Gly	Phe	Ser	Thr	Ala	Ser	Gly	Lys		
	2050					2055					2060						
Gln	Val	Ser	Ile	Leu	Glu	Ser	Ser	Leu	His	Lys	Val	Lys	Gly	Val	Leu		
2065					2070					2075					2080		
Glu	Glu	Phe	Asp	Leu	Ile	Arg	Thr	Glu	His	Ser	Leu	His	Tyr	Ser	Pro		
				2085					2090					2095			
Thr	Ser	Arg	Gln	Asn	Val	Ser	Lys	Ile	Leu	Pro	Arg	Val	Asp	Lys	Arg		
			2100					2105					2110				
Asn	Pro	Glu	His	Cys	Val	Asn	Ser	Glu	Met	Glu	Lys	Thr	Cys	Ser	Lys		
		2115					2120					2125					
Glu	Phe	Lys	Leu	Ser	Asn	Asn	Leu	Asn	Val	Glu	Gly	Gly	Ser	Ser	Glu		
	2130					2135					2140						
Asn	Asn	His	Ser	Ile	Lys	Val	Ser	Pro	Tyr	Leu	Ser	Gln	Phe	Gln	Gln		
2145					2150					2155					2160		
Asp	Lys	Gln	Gln	Leu	Val	Leu	Gly	Thr	Lys	Val	Ser	Leu	Val	Glu	Asn		
				2165					2170					2175			
Ile	His	Val	Leu	Gly	Lys	Glu	Gln	Ala	Ser	Pro	Lys	Asn	Val	Lys	Met		
			2180					2185					2190				
Glu	Ile	Gly	Lys	Thr	Glu	Thr	Phe	Ser	Asp	Val	Pro	Val	Lys	Thr	Asn		
		2195					2200					2205					
Ile	Glu	Val	Cys	Ser	Thr	Tyr	Ser	Lys	Asp	Ser	Glu	Asn	Tyr	Phe	Glu		
	2210					2215					2220						
Thr	Glu	Ala	Val	Glu	Ile	Ala	Lys	Ala	Phe	Met	Glu	Asp	Asp	Glu	Leu		
2225					2230					2235					2240		
Thr	Asp	Ser	Lys	Leu	Pro	Ser	His	Ala	Thr	His	Ser	Leu	Phe	Thr	Cys		
				2245					2250					2255			
Pro	Glu	Asn	Glu	Glu	Met	Val	Leu	Ser	Asn	Ser	Arg	Ile	Gly	Lys	Arg		
			2260														

Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe  
 2405 2410 2415  
 His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg  
 2420 2425 2430  
 Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys  
 2435 2440 2445  
 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln  
 2450 2455 2460  
 Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu  
 2465 2470 2475 2480  
 Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys  
 2485 2490 2495  
 Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu  
 2500 2505 2510  
 Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly  
 2515 2520 2525  
 Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly  
 2530 2535 2540  
 Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe  
 2545 2550 2555 2560  
 Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly  
 2565 2570 2575  
 Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp  
 2580 2585 2590  
 Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro  
 2595 2600 2605  
 Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr  
 2610 2615 2620  
 Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys  
 2625 2630 2635 2640  
 Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu  
 2645 2650 2655  
 Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile  
 2660 2665 2670  
 Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu  
 2675 2680 2685  
 Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser  
 2690 2695 2700  
 Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu  
 2705 2710 2715 2720  
 Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu  
 2725 2730 2735  
 Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile  
 2740 2745 2750  
 Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu  
 2755 2760 2765  
 Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg  
 2770 2775 2780  
 Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro  
 2785 2790 2795 2800  
 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly  
 2805 2810 2815  
 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu  
 2820 2825 2830  
 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu  
 2835 2840 2845  
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala

2850	2855	2860
Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr		
2865	2870	2875
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg		2880
	2885	2890
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala		2895
	2900	2905
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala		2910
	2915	2920
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile		2925
	2930	2935
Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln		2940
2945	2950	2955
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser		2960
	2965	2970
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro		2975
	2980	2985
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile		2990
	2995	3000
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn		3005
	3010	3015
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val		3020
3025	3030	3035
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His		3040
	3045	3050
Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val		3055
	3060	3065
Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala		3070
	3075	3080
Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys		3085
	3090	3095
Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile		3100
3105	3110	3115
Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu		3120
	3125	3130
Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu		3135
	3140	3145
Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn		3150
	3155	3160
Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu		3165
	3170	3175
His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser		3180
3185	3190	3195
Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu		3200
	3205	3210
Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu		3215
	3220	3225
Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met		3230
	3235	3240
Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn		3245
	3250	3255
Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro		3260
3265	3270	3275
Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys		3280
	3285	3290
Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile		3295
	3300	3305
		3310

Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe  
           3315                          3320                          3325  
 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu  
           3330                          3335                          3340  
 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys  
 3345                          3350                          3355                          3360  
 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser  
                           3365                          3370                          3375  
 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys  
                           3380                          3385                          3390  
 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys  
           3395                          3400                          3405  
 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile  
           3410                          3415

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI5)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC	60
TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTCGCC GCCGGGAGAA GCGTGAGGGG	120
ACAGATTTGT GACCGGCGCG GTTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT	180
CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT	237
Met Pro Ile	
1	
GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC	285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys	
5 10 15	
AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT	333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu	
20 25 30 35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA	381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	
40 45 50	
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG	429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	
55 60 65	
AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG	477

Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile	Phe	Lys	Glu	
	70						75					80				
CAA	GGG	CTG	ACT	CTG	CCG	CTG	TAC	CAA	TCT	CCT	GTA	AAA	GAA	TTA	GAT	525
Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys	Glu	Leu	Asp	
	85					90				95						
AAA	TTC	AAA	TTA	GAC	TTA	GGA	AGG	AAT	GTT	CCC	AAT	AGT	AGA	CAT	AAA	573
Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser	Arg	His	Lys	
100					105					110					115	
AGT	CTT	CGC	ACA	GTG	AAA	ACT	AAA	ATG	GAT	CAA	GCA	GAT	GAT	GTT	TCC	621
Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp	Asp	Val	Ser	
				120					125					130		
TGT	CCA	CTT	CTA	AAT	TCT	TGT	CTT	AGT	GAA	AGT	CCT	GTT	GTT	CTA	CAA	669
Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val	Val	Leu	Gln	
			135					140					145			
TGT	ACA	CAT	GTA	ACA	CCA	CAA	AGA	GAT	AAG	TCA	GTG	GTA	TGT	GGG	AGT	717
Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val	Cys	Gly	Ser	
		150					155					160				
TTG	TTT	CAT	ACA	CCA	AAG	TTT	GTG	AAG	GGT	CGT	CAG	ACA	CCA	AAA	CAT	765
Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr	Pro	Lys	His	
	165					170					175					
ATT	TCT	GAA	AGT	CTA	GGA	GCT	GAG	GTG	GAT	CCT	GAT	ATG	TCT	TGG	TCA	813
Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met	Ser	Trp	Ser	
180					185					190					195	
AGT	TCT	TTA	GCT	ACA	CCA	CCC	ACC	CTT	AGT	TCT	ACT	GTG	CTC	ATA	GTC	861
Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val	Leu	Ile	Val	
				200					205					210		
AGA	AAT	GAA	GAA	GCA	TCT	GAA	ACT	GTA	TTT	CCT	CAT	GAT	ACT	ACT	GCT	909
Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp	Thr	Thr	Ala	
			215					220					225			
AAT	GTG	AAA	AGC	TAT	TTT	TCC	AAT	CAT	GAT	GAA	AGT	CTG	AAG	AAA	AAT	957
Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu	Lys	Lys	Asn	
		230					235					240				
GAT	AGA	TTT	ATC	GCT	TCT	GTG	ACA	GAC	AGT	GAA	AAC	ACA	AAT	CAA	AGA	1005
Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr	Asn	Gln	Arg	
	245					250					255					
GAA	GCT	GCA	AGT	CAT	GGA	TTT	GGA	AAA	ACA	TCA	GGG	AAT	TCA	TTT	AAA	1053
Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn	Ser	Phe	Lys	
260					265					270					275	
GTA	AAT	AGC	TGC	AAA	GAC	CAC	ATT	GGA	AAG	TCA	ATG	CCA	CAT	GTC	CTA	1101
Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro	His	Val	Leu	
				280					285					290		
GAA	GAT	GAA	GTA	TAT	GAA	ACA	GTT	GTA	GAT	ACC	TCT	GAA	GAA	GAT	AGT	1149
Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu	Glu	Asp	Ser	

295					300					305						
TTT	TCA	TTA	TGT	TTT	TCT	AAA	TGT	AGA	ACA	AAA	AAT	CTA	CAA	AAA	GTA	1197
Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu	Gln	Lys	Val	
		310					315					320				
AGA	ACT	AGC	AAG	ACT	AGG	AAA	AAA	ATT	TTC	CAT	GAA	GCA	AAC	GCT	GAT	1245
Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala	Asn	Ala	Asp	
		325					330					335				
GAA	TGT	GAA	AAA	TCT	AAA	AAC	CAA	GTG	AAA	GAA	AAA	TAC	TCA	TTT	GTA	1293
Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr	Ser	Phe	Val	
340							345					350			355	
TCT	GAA	GTG	GAA	CCA	AAT	GAT	ACT	GAT	CCA	TTA	GAT	TCA	AAT	GTA	GCA	1341
Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser	Asn	Val	Ala	
				360					365						370	
CAT	CAG	AAG	CCC	TTT	GAG	AGT	GGA	AGT	GAC	AAA	ATC	TCC	AAG	GAA	GTT	1389
His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser	Lys	Glu	Val	
			375						380						385	
GTA	CCG	TCT	TTG	GCC	TGT	GAA	TGG	TCT	CAA	CTA	ACC	CTT	TCA	GGT	CTA	1437
Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu	Ser	Gly	Leu	
			390						395						400	
AAT	GGA	GCC	CAG	ATG	GAG	AAA	ATA	CCC	CTA	TTG	CAT	ATT	TCT	TCA	TGT	1485
Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile	Ser	Ser	Cys	
			405				410									
GAC	CAA	AAT	ATT	TCA	GAA	AAA	GAC	CTA	TTA	GAC	ACA	GAG	AAC	AAA	AGA	1533
Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu	Asn	Lys	Arg	
420							425					430			435	
AAG	AAA	GAT	TTT	CTT	ACT	TCA	GAG	AAT	TCT	TTG	CCA	CGT	ATT	TCT	AGC	1581
Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg	Ile	Ser	Ser	
				440					445						450	
CTA	CCA	AAA	TCG	GAG	AAG	CCA	TTA	AAT	GAG	GAA	ACA	GTG	GTA	AAT	AAG	1629
Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val	Val	Asn	Lys	
			455						460						465	
AGA	GAT	GAA	GAG	CAG	CAT	CTT	GAA	TCT	CAT	ACA	GAC	TGC	ATT	CTT	GCA	1677
Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys	Ile	Leu	Ala	
			470				475					480				
GTA	AAG	CAG	GCA	ATA	TCT	GGA	ACT	TCT	CCA	GTG	GCT	TCT	TCA	TTT	CAG	1725
Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser	Ser	Phe	Gln	
			485				490					495				
GGT	ATC	AAA	AAG	TCT	ATA	TTC	AGA	ATA	AGA	GAA	TCA	CCT	AAA	GAG	ACT	1773
Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro	Lys	Glu	Thr	
500							505					510			515	
TTC	AAT	GCA	AGT	TTT	TCA	GGT	CAT	ATG	ACT	GAT	CCA	AAC	TTT	AAA	AAA	1821
Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn	Phe	Lys	Lys	
				520					525						530	

GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA	1869
Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser	
535 540 545	
CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG	1917
Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp	
550 555 560	
CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA	1965
Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu	
565 570 575	
ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT	2013
Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His	
580 585 590 595	
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA	2061
Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser	
600 605 610	
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA	2109
Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala	
615 620 625	
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG	2157
Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val	
630 635 640	
AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA	2205
Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu	
645 650 655	
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA	2253
Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr	
660 665 670 675	
TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA	2301
Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala	
680 685 690	
AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT	2349
Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp	
695 700 705	
TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC	2397
Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser	
710 715 720	
AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC	2445
Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His	
725 730 735	
CCA GTA CAA CAC TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC	2493
Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser	
740 745 750 755	

CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA	2541
Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu	
760 765 770	
ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA	2589
Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg	
775 780 785	
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT	2637
Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr	
790 795 800	
GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA	2685
Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln	
805 810 815	
GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA	2733
Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro	
820 825 830 835	
CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC	2781
Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe	
840 845 850	
AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT	2829
Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr	
855 860 865	
ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC	2877
Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Leu Phe	
870 875 880	
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA ATA GCT AAT GAA AGG AAT	2925
Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Ile Ala Asn Glu Arg Asn	
885 890 895	
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT	2973
Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr	
900 905 910 915	
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA	3021
Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly	
920 925 930	
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG	3069
Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu	
935 940 945	
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA	3117
Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile	
950 955 960	
AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA	3165
Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile	
965 970 975	
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG GAC AAA TGG GCA GGA	3213



Asp 980	Lys	Ile	Pro	Glu	Lys 985	Asn	Asn	Asp	Tyr	Met 990	Asp	Lys	Trp	Ala	Gly 995		
CTC Leu	TTA Leu	GGT Gly	CCA Pro	ATT Ile	TCA Ser	AAT Asn	CAC His	AGT Ser	TTT Phe	GGA Gly	GGT Gly	AGC Ser	TTC Phe	AGA Arg	ACA Thr	3261	
				1000						1005						1010	
GCT Ala	TCA Ser	AAT Asn	AAG Lys	GAA Glu	ATC Ile	AAG Lys	CTC Leu	TCT Ser	GAA Glu	CAT His	AAC Asn	ATT Ile	AAG Lys	AAG Lys	AGC Ser	3309	
				1015						1020						1025	
AAA Lys	ATG Met	TTC Phe	TTC Phe	AAA Lys	GAT Asp	ATT Ile	GAA Glu	GAA Glu	CAA Gln	TAT Tyr	CCT Pro	ACT Thr	AGT Ser	TTA Leu	GCT Ala	3357	
				1030						1035						1040	
TGT Cys	GTT Val	GAA Glu	ATT Ile	GTA Val	AAT Asn	ACC Thr	TTG Leu	GCA Ala	TTA Leu	GAT Asp	AAT Asn	CAA Gln	AAG Lys	AAA Lys	CTG Leu	3405	
						1050								1055			
AGC Ser	AAG Lys	CCT Pro	CAG Gln	TCA Ser	ATT Ile	AAT Asn	ACT Thr	GTA Val	TCT Ser	GCA Ala	CAT His	TTA Leu	CAG Gln	AGT Ser	AGT Ser	3453	
1060						1065								1070		1075	
GTA Val	GTT Val	GTT Val	TCT Ser	GAT Asp	TGT Cys	AAA Lys	AAT Asn	AGT Ser	CAT His	ATA Ile	ACC Thr	CCT Pro	CAG Gln	ATG Met	TTA Leu	3501	
				1080						1085						1090	
TTT Phe	TCC Ser	AAG Lys	CAG Gln	GAT Asp	TTT Phe	AAT Asn	TCA Ser	AAC Asn	CAT His	AAT Asn	TTA Leu	ACA Thr	CCT Pro	AGC Ser	CAA Gln	3549	
				1095						1100						1105	
AAG Lys	GCA Ala	GAA Glu	ATT Ile	ACA Thr	GAA Glu	CTT Leu	TCT Ser	ACT Thr	ATA Ile	TTA Leu	GAA Glu	GAA Glu	TCA Ser	GGA Gly	AGT Ser	3597	
				1110						1115						1120	
CAG Gln	TTT Phe	GAA Glu	TTT Phe	ACT Thr	CAG Gln	TTT Phe	AGA Arg	AAA Lys	CCA Pro	AGC Ser	TAC Tyr	ATA Ile	TTG Leu	CAG Gln	AAG Lys	3645	
				1125						1130						1135	
AGT Ser	ACA Thr	TTT Phe	GAA Glu	GTG Val	CCT Pro	GAA Glu	AAC Asn	CAG Gln	ATG Met	ACT Thr	ATC Ile	TTA Leu	AAG Lys	ACC Thr	ACT Thr	3693	
1140						1145								1150		1155	
TCT Ser	GAG Glu	GAA Glu	TGC Cys	AGA Arg	GAT Asp	GCT Ala	GAT Asp	CTT Leu	CAT His	GTC Val	ATA Ile	ATG Met	AAT Asn	GCC Ala	CCA Pro	3741	
				1160						1165						1170	
TCG Ser	ATT Ile	GGT Gly	CAG Gln	GTA Val	GAC Asp	AGC Ser	AGC Ser	AAG Lys	CAA Gln	TTT Phe	GAA Glu	GGT Gly	ACA Thr	GTT Val	GAA Glu	3789	
				1175						1180						1185	
ATT Ile	AAA Lys	CGG Arg	AAG Lys	TTT Phe	GCT Ala	GGC Gly	CTG Leu	TTG Leu	AAA Lys	AAT Asn	GAC Asp	TGT Cys	AAC Asn	AAA Lys	AGT Ser	3837	
				1190						1195						1200	
GCT Ala	TCT Ser	GGT Gly	TAT Tyr	TTA Leu	ACA Thr	GAT Asp	GAA Glu	AAT Asn	GAA Glu	GTG Val	GGG Gly	TTT Phe	AGG Arg	GGC Gly	TTT Phe	3885	

1205	1210	1215	
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA			3933
Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln			
1220	1225	1230	1235
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT			3981
Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr			
	1240	1245	1250
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT			4029
Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp			
	1255	1260	1265
TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA			4077
Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val			
	1270	1275	1280
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA			4125
Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu			
	1285	1290	1295
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA			4173
Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg			
1300	1305	1310	1315
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT			4221
Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser			
	1320	1325	1330
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT			4269
His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val			
	1335	1340	1345
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC			4317
Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn			
	1350	1355	1360
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG			4365
Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln			
	1365	1370	1375
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT			4413
Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala			
1380	1385	1390	1395
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT			4461
Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala			
	1400	1405	1410
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT			4509
Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe			
	1415	1420	1425
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT			4557
Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe			
	1430	1435	1440

AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn 1445 1450 1455	4605
TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met 1460 1465 1470 1475	4653
GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu 1480 1485 1490	4701
AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln 1495 1500 1505	4749
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly 1510 1515 1520	4797
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu 1525 1530 1535	4845
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu 1540 1545 1550 1555	4893
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu 1560 1565 1570	4941
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala 1575 1580 1585	4989
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn 1590 1595 1600	5037
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn 1605 1610 1615	5085
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu 1620 1625 1630 1635	5133
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro 1640 1645 1650	5181
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser 1655 1660 1665	5229

GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln 1670 1675 1680	5277
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp 1685 1690 1695	5325
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu 1700 1705 1710 1715	5373
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His 1720 1725 1730	5421
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn 1735 1740 1745	5469
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu 1750 1755 1760	5517
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val 1765 1770 1775	5565
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys 1780 1785 1790 1795	5613
GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu 1800 1805 1810	5661
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile 1815 1820 1825	5709
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala 1830 1835 1840	5757
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile 1845 1850 1855	5805
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys 1860 1865 1870 1875	5853
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala 1880 1885 1890	5901
GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT	5949

Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser	
1895 1900 1905	
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC	5997
Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp	
1910 1915 1920	
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG	6045
Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu	
1925 1930 1935	
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA	6093
Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser	
1940 1945 1950 1955	
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT	6141
Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser	
1960 1965 1970	
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG	6189
Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln	
1975 1980 1985	
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA	6237
Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile	
1990 1995 2000	
GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC	6285
Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn	
2005 2010 2015	
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT	6333
Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr	
2020 2025 2030 2035	
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT	6381
Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn	
2040 2045 2050	
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC	6429
Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser	
2055 2060 2065	
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT	6477
Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe	
2070 2075 2080	
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA	6525
Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg	
2085 2090 2095	
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG	6573
Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu	
2100 2105 2110 2115	
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA	6621
His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys	

	2120	2125	2130	
	TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC			6669
	Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His			
	2135	2140	2145	
	TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA			6717
	Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln			
	2150	2155	2160	
	CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT			6765
	Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val			
	2165	2170	2175	
	TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT			6813
2180	Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly			
	2185	2190	2195	
	AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT			6861
	Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val			
	2200	2205	2210	
	TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA			6909
	Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala			
	2215	2220	2225	
	GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT			6957
	Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser			
	2230	2235	2240	
	AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT			7005
	Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn			
	2245	2250	2255	
	GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG			7053
2260	Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu			
	2265	2270	2275	
	CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT			7101
	Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn			
	2280	2285	2290	
	GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA			7149
	Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser			
	2295	2300	2305	
	AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT			7197
	Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His			
	2310	2315	2320	
	CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG			7245
	His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys			
	2325	2330	2335	
	GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA			7293
2340	Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu			
	2345	2350	2355	

TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser 2360 2365 2370	7341
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala 2375 2380 2385	7389
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr 2390 2395 2400	7437
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val 2405 2410 2415	7485
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln 2420 2425 2430 2435	7533
AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp 2440 2445 2450	7581
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala 2455 2460 2465	7629
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser 2470 2475 2480	7677
CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln 2485 2490 2495	7725
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr 2500 2505 2510 2515	7773
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val 2520 2525 2530	7821
CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys 2535 2540 2545	7869
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His 2550 2555 2560	7917
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile 2565 2570 2575	7965

CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala 2580 2585 2590 2595	8013
GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp 2600 2605 2610	8061
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile 2615 2620 2625	8109
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala 2630 2635 2640	8157
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg 2645 2650 2655	8205
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile 2660 2665 2670 2675	8253
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser 2680 2685 2690	8301
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys 2695 2700 2705	8349
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp 2710 2715 2720	8397
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val 2725 2730 2735	8445
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly 2740 2745 2750 2755	8493
GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro 2760 2765 2770	8541
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg 2775 2780 2785	8589
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu 2790 2795 2800	8637
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT	8685



Pro	Leu	Ser	Ser	Leu	Phe	Ser	Asp	Gly	Gly	Asn	Val	Gly	Cys	Val	Asp	
2805						2810					2815					
GTA	ATT	ATT	CAA	AGA	GCA	TAC	CCT	ATA	CAG	TGG	ATG	GAG	AAG	ACA	TCA	8733
Val	Ile	Ile	Gln	Arg	Ala	Tyr	Pro	Ile	Gln	Trp	Met	Glu	Lys	Thr	Ser	
2820					2825					2830					2835	
TCT	GGA	TTA	TAC	ATA	TTT	CGC	AAT	GAA	AGA	GAG	GAA	GAA	AAG	GAA	GCA	8781
Ser	Gly	Leu	Tyr	Ile	Phe	Arg	Asn	Glu	Arg	Glu	Glu	Glu	Lys	Glu	Ala	
				2840					2845					2850		
GCA	AAA	TAT	GTG	GAG	GCC	CAA	CAA	AAG	AGA	CTA	GAA	GCC	TTA	TTC	ACT	8829
Ala	Lys	Tyr	Val	Glu	Ala	Gln	Gln	Lys	Arg	Leu	Glu	Ala	Leu	Phe	Thr	
			2855					2860					2865			
AAA	ATT	CAG	GAG	GAA	TTT	GAA	GAA	CAT	GAA	GAA	AAC	ACA	ACA	AAA	CCA	8877
Lys	Ile	Gln	Glu	Glu	Phe	Glu	Glu	His	Glu	Glu	Asn	Thr	Thr	Lys	Pro	
	2870						2875				2880					
TAT	TTA	CCA	TCA	CGT	GCA	CTA	ACA	AGA	CAG	CAA	GTT	CGT	GCT	TTG	CAA	8925
Tyr	Leu	Pro	Ser	Arg	Ala	Leu	Thr	Arg	Gln	Gln	Val	Arg	Ala	Leu	Gln	
	2885					2890					2895					
GAT	GGT	GCA	GAG	CTT	TAT	GAA	GCA	GTG	AAG	AAT	GCA	GCA	GAC	CCA	GCT	8973
Asp	Gly	Ala	Glu	Leu	Tyr	Glu	Ala	Val	Lys	Asn	Ala	Ala	Asp	Pro	Ala	
2900				2905					2910					2915		
TAC	CTT	GAG	GGT	TAT	TTC	AGT	GAA	GAG	CAG	TTA	AGA	GCC	TTG	AAT	AAT	9021
Tyr	Leu	Glu	Gly	Tyr	Phe	Ser	Glu	Glu	Gln	Leu	Arg	Ala	Leu	Asn	Asn	
			2920						2925				2930			
CAC	AGG	CAA	ATG	TTG	AAT	GAT	AAG	AAA	CAA	GCT	CAG	ATC	CAG	TTG	GAA	9069
His	Arg	Gln	Met	Leu	Asn	Asp	Lys	Lys	Gln	Ala	Gln	Ile	Gln	Leu	Glu	
		2935						2940				2945				
ATT	AGG	AAG	ACC	ATG	GAA	TCT	GCT	GAA	CAA	AAG	GAA	CAA	GGT	TTA	TCA	9117
Ile	Arg	Lys	Thr	Met	Glu	Ser	Ala	Glu	Gln	Lys	Glu	Gln	Gly	Leu	Ser	
	2950						2955				2960					
AGG	GAT	GTC	ACA	ACC	GTG	TGG	AAG	TTG	CGT	ATT	GTA	AGC	TAT	TCA	AAA	9165
Arg	Asp	Val	Thr	Thr	Val	Trp	Lys	Leu	Arg	Ile	Val	Ser	Tyr	Ser	Lys	
	2965					2970				2975						
AAA	GAA	AAA	GAT	TCA	GTT	ATA	CTG	AGT	ATT	TGG	CGT	CCA	TCA	TCA	GAT	9213
Lys	Glu	Lys	Asp	Ser	Val	Ile	Leu	Ser	Ile	Trp	Arg	Pro	Ser	Ser	Asp	
2980				2985					2990				2995			
TTA	TAT	TCT	CTG	TTA	ACA	GAA	GGA	AAG	AGA	TAC	AGA	ATT	TAT	CAT	CTT	9261
Leu	Tyr	Ser	Leu	Leu	Thr	Glu	Gly	Lys	Arg	Tyr	Arg	Ile	Tyr	His	Leu	
			3000						3005				3010			
GCA	ACT	TCA	AAA	TCT	AAA	AGT	AAA	TCT	GAA	AGA	GCT	AAC	ATA	CAG	TTA	9309
Ala	Thr	Ser	Lys	Ser	Lys	Ser	Lys	Ser	Glu	Arg	Ala	Asn	Ile	Gln	Leu	
		3015					3020				3025					
GCA	GCG	ACA	AAA	AAA	ACT	CAG	TAT	CAA	CAA	CTA	CCG	GTT	TCA	GAT	GAA	9357
Ala	Ala	Thr	Lys	Lys	Thr	Gln	Tyr	Gln	Gln	Leu	Pro	Val	Ser	Asp	Glu	

3030	3035	3040	
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys 3045 3050 3055			9405
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile 3060 3065 3070 3075			9453
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val 3080 3085 3090			9501
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile 3095 3100 3105			9549
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser 3110 3115 3120			9597
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe 3125 3130 3135			9645
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe 3140 3145 3150 3155			9693
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile 3160 3165 3170			9741
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn 3175 3180 3185			9789
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr 3190 3195 3200			9837
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser 3205 3210 3215			9885
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala 3220 3225 3230 3235			9933
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys 3240 3245 3250			9981
TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys 3255 3260 3265			10029

AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT	10077
Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val	
3270 3275 3280	
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG	10125
Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln	
3285 3290 3295	
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA	10173
Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys	
3300 3305 3310 3315	
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT	10221
Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile	
3320 3325 3330	
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA	10269
Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile	
3335 3340 3345	
AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA	10317
Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile	
3350 3355 3360	
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT	10365
Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr	
3365 3370 3375	
CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG	10413
Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu	
3380 3385 3390 3395	
AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA	10461
Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr	
3400 3405 3410	
ATT ACA ACT AAA AAA TAT ATC TAA	10485
Ile Thr Thr Lys Lys Tyr Ile	
3415	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Pro	Ile	Gly	Ser	Lys	Glu	Arg	Pro	Thr	Phe	Phe	Glu	Ile	Phe	Lys
1				5				10					15		

Thr	Arg	Cys	Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe	
			20					25					30			
Glu	Glu	Leu	Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu	
		35					40					45				
Glu	Ser	Glu	His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr	
	50				55						60					
Pro	Gln	Arg	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile	
65					70					75					80	
Phe	Lys	Glu	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys	
				85					90					95		
Glu	Leu	Asp	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser	
			100					105					110			
Arg	His	Lys	Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp	
		115					120					125				
Asp	Val	Ser	Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val	
	130					135					140					
Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val	
145					150					155					160	
Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr	
				165					170					175		
Pro	Lys	His	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met	
			180					185					190			
Ser	Trp	Ser	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val	
		195					200					205				
Leu	Ile	Val	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp	
	210					215					220					
Thr	Thr	Ala	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu	
225					230					235					240	
Lys	Lys	Asn	Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr	
			245						250					255		
Asn	Gln	Arg	Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn	
			260					265					270			
Ser	Phe	Lys	Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro	
		275					280					285				
His	Val	Leu	Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu	
	290					295					300					
Glu	Asp	Ser	Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu	
305					310					315					320	
Gln	Lys	Val	Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala	
				325					330					335		
Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr	
			340					345					350			
Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser	
		355					360					365				
Asn	Val	Ala	His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser	
	370					375						380				
Lys	Glu	Val	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu	
385					390					395					400	
Ser	Gly	Leu	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile	
			405						410					415		
Ser	Ser	Cys	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu	
			420					425					430			
Asn	Lys	Arg	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg	
		435					440					445				
Ile	Ser	Ser	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val	
	450					455					460					
Val	Asn	Lys	Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys	

465					470					475				480	
Ile	Leu	Ala	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser
				485					490					495	
Ser	Phe	Gln	Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro
			500					505					510		
Lys	Glu	Thr	Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn
		515					520					525			
Phe	Lys	Lys	Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr
	530					535					540				
Val	Cys	Ser	Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn
545					550					555					560
Gly	Ser	Trp	Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn
				565					570					575	
Ala	Gly	Leu	Ile	Ser	Thr	Leu	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr	
			580					585					590		
Ala	Ile	His	Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp
		595					600					605			
Gln	Lys	Ser	Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala
	610					615					620				
Phe	Glu	Ala	Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His
625					630					635					640
Ser	Ser	Val	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr
				645					650					655	
Leu	Ser	Leu	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg
			660					665					670		
Asn	Glu	Thr	Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr
		675					680					685			
Lys	Glu	Ala	Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro
	690					695					700				
Glu	Ala	Asp	Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp
705					710					715					720
Pro	Lys	Ser	Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala
				725					730					735	
Ala	Cys	His	Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp
			740					745					750		
Phe	Gln	Ser	Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr
		755					760					765			
Leu	Ile	Leu	Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met
	770					775					780				
Ile	Ser	Arg	Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly
785				790					795						800
Asn	Asn	Tyr	Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu
				805					810					815	
Lys	Asn	Gln	Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu
			820					825					830		
Leu	Leu	Pro	Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys
		835					840					845			
Val	Gln	Phe	Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln
	850					855					860				
Glu	Glu	Thr	Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu
865					870					875					880
Glu	Leu	Phe	Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Ile	Ala	Asn
				885					890					895	
Glu	Arg	Asn	Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu	Leu	His	Glu	Thr
		900					905						910		
Asp	Leu	Thr	Cys	Val	Asn	Glu	Pro	Ile	Phe	Lys	Asn	Ser	Thr	Met	Val
		915					920					925			

Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys  
 930 935 940  
 Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys  
 945 950 955 960  
 Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser  
 965 970 975  
 Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys  
 980 985 990  
 Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser  
 995 1000 1005  
 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile  
 1010 1015 1020  
 Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr  
 1025 1030 1035 1040  
 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln  
 1045 1050 1055  
 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu  
 1060 1065 1070  
 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro  
 1075 1080 1085  
 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr  
 1090 1095 1100  
 Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu  
 1105 1110 1115 112  
 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile  
 1125 1130 1135  
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu  
 1140 1145 1150  
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met  
 1155 1160 1165  
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly  
 1170 1175 1180  
 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys  
 1185 1190 1195 1200  
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe  
 1205 1210 1215  
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu  
 1220 1225 1230  
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser  
 1235 1240 1245  
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys  
 1250 1255 1260  
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp  
 1265 1270 1275 1280  
 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn  
 1285 1290 1295  
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn  
 1300 1305 1310  
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser  
 1315 1320 1325  
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn  
 1330 1335 1340  
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp  
 1345 1350 1355 1360  
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly  
 1365 1370 1375  
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val



Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His  
 1845 1850 1855  
 Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys  
 1860 1865 1870  
 Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys  
 1875 1880 1885  
 Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu  
 1890 1895 1900  
 His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val  
 1905 1910 1915 1920  
 Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met  
 1925 1930 1935  
 Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu  
 1940 1945 1950  
 Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser  
 1955 1960 1965  
 Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys  
 1970 1975 1980  
 Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe  
 1985 1990 1995 2000  
 Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe  
 2005 2010 2015  
 Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala  
 2020 2025 2030  
 Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn  
 2035 2040 2045  
 Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys  
 2050 2055 2060  
 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu  
 2065 2070 2075 2080  
 Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro  
 2085 2090 2095  
 Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg  
 2100 2105 2110  
 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys  
 2115 2120 2125  
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu  
 2130 2135 2140  
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln  
 2145 2150 2155 2160  
 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn  
 2165 2170 2175  
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met  
 2180 2185 2190  
 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn  
 2195 2200 2205  
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu  
 2210 2215 2220  
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu  
 2225 2230 2235 2240  
 Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys  
 2245 2250 2255  
 Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg  
 2260 2265 2270  
 Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn  
 2275 2280 2285  
 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu



2290	2295	2300
Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu		
2305	2310	2315
Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg		2320
	2325	2330
Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro		2335
	2340	2345
Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu		2350
	2355	2360
Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln		2365
	2370	2375
Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly		2380
2385	2390	2395
Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe		2400
	2405	2410
His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg		2415
	2420	2425
Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys		2430
	2435	2440
Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln		2445
	2450	2455
Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu		2460
2465	2470	2475
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys		2480
	2485	2490
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu		2495
	2500	2505
Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly		2510
	2515	2520
Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly		2525
	2530	2535
Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe		2540
2545	2550	2555
Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly		2560
	2565	2570
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp		2575
	2580	2585
Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro		2590
	2595	2600
Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr		2605
	2610	2615
Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys		2620
2625	2630	2635
Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu		2640
	2645	2650
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile		2655
	2660	2665
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu		2670
	2675	2680
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser		2685
	2690	2695
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu		2700
2705	2710	2715
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu		2720
	2725	2730
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile		2735
	2740	2745
		2750

Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu  
 2755 2760 2765  
 Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg  
 2770 2775 2780  
 Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro  
 2785 2790 2795 2800  
 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly  
 2805 2810 2815  
 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu  
 2820 2825 2830  
 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu  
 2835 2840 2845  
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala  
 2850 2855 2860  
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr  
 2865 2870 2875 2880  
 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg  
 2885 2890 2895  
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala  
 2900 2905 2910  
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala  
 2915 2920 2925  
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile  
 2930 2935 2940  
 Gln Leu Glu Ile Arg Lys Thr Met Glu Ser Ala Glu Gln Lys Glu Gln  
 2945 2950 2955 2960  
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser  
 2965 2970 2975  
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro  
 2980 2985 2990  
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile  
 2995 3000 3005  
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn  
 3010 3015 3020  
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val  
 3025 3030 3035 3040  
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His  
 3045 3050 3055  
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val  
 3060 3065 3070  
 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala  
 3075 3080 3085  
 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys  
 3090 3095 3100  
 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile  
 3105 3110 3115 3120  
 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu  
 3125 3130 3135  
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu  
 3140 3145 3150  
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn  
 3155 3160 3165  
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu  
 3170 3175 3180  
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser  
 3185 3190 3195 3200  
 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu

				3205					3210					3215					
Met	Ser	Ser	Pro	Asn	Cys	Glu	Ile	Tyr	Tyr	Gln	Ser	Pro	Leu	Ser	Leu				
			3220						3225					3230					
Cys	Met	Ala	Lys	Arg	Lys	Ser	Val	Ser	Thr	Pro	Val	Ser	Ala	Gln	Met				
		3235					3240						3245						
Thr	Ser	Lys	Ser	Cys	Lys	Gly	Glu	Lys	Glu	Ile	Asp	Asp	Gln	Lys	Asn				
		3250				3255						3260							
Cys	Lys	Lys	Arg	Arg	Ala	Leu	Asp	Phe	Leu	Ser	Arg	Leu	Pro	Leu	Pro				
3265					3270					3275					3280				
Pro	Pro	Val	Ser	Pro	Ile	Cys	Thr	Phe	Val	Ser	Pro	Ala	Ala	Gln	Lys				
			3285						3290					3295					
Ala	Phe	Gln	Pro	Pro	Arg	Ser	Cys	Gly	Thr	Lys	Tyr	Glu	Thr	Pro	Ile				
		3300						3305					3310						
Lys	Lys	Lys	Glu	Leu	Asn	Ser	Pro	Gln	Met	Thr	Pro	Phe	Lys	Lys	Phe				
		3315				3320					3325								
Asn	Glu	Ile	Ser	Leu	Leu	Glu	Ser	Asn	Ser	Ile	Ala	Asp	Glu	Glu	Leu				
		3330				3335					3340								
Ala	Leu	Ile	Asn	Thr	Gln	Ala	Leu	Leu	Ser	Gly	Ser	Thr	Gly	Glu	Lys				
3345					3350					3355					3360				
Gln	Phe	Ile	Ser	Val	Ser	Glu	Ser	Thr	Arg	Thr	Ala	Pro	Thr	Ser	Ser				
			3365					3370					3375						
Glu	Asp	Tyr	Leu	Arg	Leu	Lys	Arg	Arg	Cys	Thr	Thr	Ser	Leu	Ile	Lys				
		3380				3385						3390							
Glu	Gln	Glu	Ser	Ser	Gln	Ala	Ser	Thr	Glu	Glu	Cys	Glu	Lys	Asn	Lys				
		3395				3400					3405								
Gln	Asp	Thr	Ile	Thr	Thr	Lys	Lys	Tyr	Ile										
		3410				3415													

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGAGTTTTAC CTCAGTCACA

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CAGGAAACAG CTATGACCCT GTGACGTACT GGGTTTTTTAG C

41

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 3FII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCTTTAAC TGTTCTGGGT CACA

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 3RII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCCAGCATGA CACAATTAAT GA

22

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...44

(D) OTHER INFORMATION: 4F/M 13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGTAAAACGA CGGCCAGTAG AATGCAAATT TATAATCCAG AGTA

44

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 4R-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATCAGATTCA TCTTTATAGA AC

22

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 5+6F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGTAAAACGA CGGCCAGTTG TGTGGCATT TTAAACATCA

40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...38

(D) OTHER INFORMATION: 5+6R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGGAAACAG CTATGACCCA GGGCAAAGGT ATAACGCT

38

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...38

(D) OTHER INFORMATION: 7F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGTAAAACGA CGGCCAGTTA AGTGAAATAA AGAGTGAA

38

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...36

(D) OTHER INFORMATION: 7R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAGGAAACAG CTATGACCAG AAGTATTAGA GATGAC

36

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 8F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGTAAACGA CGGCCAGTGC CATATCTTAC CACCTTGTGA

40

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 8FIA primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTGCATTCTA GTGATAATAT AC

22

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 8RIA primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AATTGTTAGC AATTTCAAC

19

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 9F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGTAAAACGA CGGCCAGTTG GACCTAGGTT GATTGCAGAT

40

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 9R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAGGAAACAG CTATGACCTA AACTGAGATC ACGGGTGACA

40

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other



- (B) LOCATION: 1...24
- (D) OTHER INFORMATION: 10AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATAATATA AATTATATGG CTTA

24

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 10AR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAGGAAACAG CTATGACCCC TAGTCTTGCT AGTTCTT

37

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...42
- (D) OTHER INFORMATION: 10BF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGTAAAACGA CGGCCAGTAR CTGAAGTGGA ACCAAATGAT AC

42

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...44
- (D) OTHER INFORMATION: 10BR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGGAAACAG CTATGACCAC GTGGCAAAGA ATTCTCTGAA GTAA

44

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 10CF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TGTAAAACGA CGGCCAGTCA GCATCTTGAA TCTCATACAG

40

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 10CRII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGACAGAGGT ACCTGAATC

19

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 11AF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGTAAACGA CGCCAGTTG GTACTTTAAT TTTGTCACTT

40

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 11AR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGGAAACAG CTATGACCTG CAGGCATGAC AGAGAAT

37

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11BF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAGAAGCAAA ATGTAATAAG GA 22

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11BR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CATTTAAAGC ACATACATCT TG 22

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: primer
- (B) LOCATION:
- (D) OTHER INFORMATION: 11CF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCTAGAGGCA AAGAATCATA C 21

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11CR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CAAGATTATT CCTTTCATTA GC 22

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11DF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AACCAAAACA CAAATCTAAG AG 22

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...23
- (D) OTHER INFORMATION: 11DR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTCATTTTTTA TATGCTGCTT TAC 23

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11EF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGTTTTATAT GGAGACACAG G

21

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...23
- (D) OTHER INFORMATION: 11ER primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTATTTACAA TTTCAACACA AGC

23

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11FF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATCACAGTTT TGGAGGTAGC

20

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11FR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTGACTTCCT GATTCTTCTA A

21

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11GF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTCAGATGTT ATTTTCCAAG C

21

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other

- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11GR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGTTAAATA ACCAGAAGCA C

21

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...18
- (D) OTHER INFORMATION: 11HF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGGTAGACAG CAGCAAGC

18

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11HR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTAATATCAG TTGGCATTTA TT

22

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11IF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TGCAGAGGTA CATCCAATAA G

21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11IR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCAGTAAA TAGCAAGTCC G

21

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...23
- (D) OTHER INFORMATION: 11JF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TACTGAAAAT GAAGATAACA AAT

23

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11JR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATTTTGTTC TTTCTTATGTC AG 22

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11KF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TGTAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA 35

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11KR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG 35

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11LF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CACAAAATAC TGAAAGAAAG TG

22

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 11LR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGCACCACAG TCTCAATAG

19

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11MF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCAAAGACCC TAAAGTACAG

20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11MR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CATCAAATAT TCCTTCTCTA AG

22

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11NF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGTAAAACGA CGGCCAGTGA AAATTCAGCC TTAGC

35

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11NR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CAGGAAACAG CTATGACCAT CAGAATGGTA GGAAT

35

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11OF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTACTATAGC TGAAAATGAC AA

22

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11OR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCACTGGCT ATCCTAAATG

20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11PF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TGAAGATATT TCGGTTGAGG

20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11PR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTCAGCAAAA ACCTTATGTG

20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11QF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACGAAAATTA TGGCAGGTTG T

21

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11QR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTTGTCTTGC GTTTTGTAAT G

21

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11RF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GCTTCATAAG TCAGTCTCAT

20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11RR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCAAATTCCT CTAACACTCC

20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11SF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TGTAAAACGA CGGCCAGTTA CAGCAAGTGG AAAGC

35

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 11SR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CAGGAAACAG CTATGACCAA GTTTCAGTTT TACCAAT

37

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11TF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTTCTTCAGA AAATAATCAC TC

22

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11TR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TGTAAAAAGA GAATGTGTGG C

21

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 11UF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTAAAACGA CGGCCAGTAC TTTTCTGAT GTTCCTGTG

39

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE  
 (A) NAME/KEY: other  
 (B) LOCATION: 1...39  
 (D) OTHER INFORMATION: 11UR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:  
 CAGGAAACAG CTATGACCTA AAAATAGTGA TTGGCAACA 39

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE  
 (A) NAME/KEY: other  
 (B) LOCATION: 1...42  
 (D) OTHER INFORMATION: 12F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:  
 TGTAAACGA CGGCCAGTAG TGGTGTTTTA AAGTGGTCAA AA 42

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE  
 (A) NAME/KEY: other  
 (B) LOCATION: 1...40  
 (D) OTHER INFORMATION: 12R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:  
CAGGAAACAG CTATGACCGG ATCCACCTGA GGTCAGAATA 40

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE  
(A) NAME/KEY: other  
(B) LOCATION: 1...21  
(D) OTHER INFORMATION: 13-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:  
TAACATTTAA GCATCCGTTA C 21

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE  
(A) NAME/KEY: other  
(B) LOCATION: 1...28  
(D) OTHER INFORMATION: 13-2R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:  
AAACGAGACT TTTCTCATAC TGTATTAG 28

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE
  - (A) NAME/KEY: other
  - (B) LOCATION: 1...22
  - (D) OTHER INFORMATION: 14F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ACCATGTAGC AAATGAGGGT CT

22

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE
  - (A) NAME/KEY: other
  - (B) LOCATION: 1...22
  - (D) OTHER INFORMATION: 14AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GCTTTTGTCT GTTTTCCTCC AA

22

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE
  - (A) NAME/KEY: other
  - (B) LOCATION: 1...21
  - (D) OTHER INFORMATION: 15-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCAGGGGTTG TGCTTTTAA A

21

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: primer
- (B) LOCATION:
- (D) OTHER INFORMATION: 15FUT/M13-R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAGGAAACAG CTATGACCAC TCTGTCATAA AAGCCATC

38

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...24
- (D) OTHER INFORMATION: 16AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTTGTTTGT TATAATTGTT TTTA

24

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 16AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CCAAC TTTT AGTTCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 17F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TTCAGTATCA TCCTATGTG

19

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 17AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGAAACCTTA ACCCATACTG

20

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other

- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 18FUT/M13-AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TGTAAAACGA CGGCCAGTGA ATTCTAGAGT CACACTTCC

39

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 18R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CAGGAAACAG CTATGACCTT TAACTGAATC AATGACTG

38

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...41
- (D) OTHER INFORMATION: 19F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TGTAAAACGA CGGCCAGTAA GTGAATATTT TTAAGGCAGT T

41

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 19FUT/M13-R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CAGGAAACAG CTATGACCAA GAGACCGAAA CTCCATCTC

39

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 20F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TGTAAAACGA CGGCCAGTCA CTGTGCCTGG CCTGATAC

38

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 20R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CAGGAAACAG CTATGACCAT GTTAAATTCA AAGTCTCTA

39

(2) INFORMATION FOR SEQ ID NO:95:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 21F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TGTAAACGA CGGCCAGTGG GTGTTTTATG CTTGGTTCT

39

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 21R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CAGGAAACAG CTATGACCCA TTTCAACATA TTCCTTCCTG

40

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19

(D) OTHER INFORMATION: 22F-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AACCACACCC TTAAGATGA

19

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 22R-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCATTAGTAG TGGATTTTGC

20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...16
- (D) OTHER INFORMATION: 23FII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCACTTCCAT TGCATC

16

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...17
- (D) OTHER INFORMATION: 23RII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TGCCAACTGG TAGCTCC

17

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 24 2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TACAGTTAGC AGCGACAAAA

20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 24R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CAGGAAACAG CTATGACCAT TTGCCAACTG GTAGCTCC

38

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 25F-7/23 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCTTTTCGCCA AATTCAGCTA

20

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 25R-7/23 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TACCAAAATG TGTGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 26-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AATCACTGAT ACTGGTTTTG

20

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 26-2R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TATACTTACA GGAGCCACAT

20

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...18
- (D) OTHER INFORMATION: 27AF-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTGTGTGTAA TATTTGCG

18

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...40

(D) OTHER INFORMATION: 27AR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CAGGAAACAG CTATGACGGC AAGTTCTTCG TCAGCTATTG

40

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...40

(D) OTHER INFORMATION: 27BF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TGTAAAACGA CGGCCAGTGA ATTCTCCTCA GATGACTCCA

40

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...38

(D) OTHER INFORMATION: 27BR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CAGGAAACAG CTATGACCTC TTTGCTCATT GTGCAACA

38

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 1...1158
- (D) OTHER INFORMATION: Exon 10, nucleotides 31-1146 correspond to nucleotides 1022-2137 of complete coding sequence

(ix) FEATURE

- (A) NAME/KEY: variable
- (B) LOCATION: 102...602
- (D) OTHER INFORMATION: M at positions 102 or 351 = A or C;  
R at position 602 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```
TTAATGTGCT TCTGTTTTAT ACTTTAACAG GATTTGGAAA AACATCAGGG AATTCATTTA 60
AAGTAAATAG CTGCAAAGAC CACATTGGAA AGTCAATGCC AMATGTCCTA GAAGATGAAG 120
TATATGAAAC AGTTGTAGAT ACCTCTGAAG AAGATAGTTT TTCATTATGT TTTTCTAAAT 180
GTAGAACAAA AAATCTACAA AAAGTAAGAA CTAGCAAGAC TAGGAAAAAA ATTTTCCATG 240
AAGCAAACGC TGATGAATGT GAAAAATCTA AAAACCAAGT GAAAGAAAAA TACTCATTG 300
TATCTGAAGT GGAACCAAT GATACTGATC CATTAGATTG AAATGTAGCA MATCAGAAGC 360
CCTTTGAGAG TGGAAGTGAC AAAATCTCCA AGGAAGTTGT ACCGTCTTTG GCCTGTGAAT 420
GGTCTCAACT AACCCTTTCA GGTCTAAATG GAGCCCAGAT GGAGAAAATA CCCCTATTGC 480
ATATTTCTTC ATGTGACCAA AATATTTTCA AAAAAGACCT ATTAGACACA GAGAACAAAA 540
GAAAGAAAGA TTTTCTTACT TCAGAGAATT CTTTGCCACG TATTTCTAGC CTACCAAAAT 600
CRGAGAAGCC ATTAAATGAG GAAACAGTGG TAAATAAGAG AGATGAAGAG CAGCATCTTG 660
AATCTCATAC AGACTGCATT CTTGCAGTAA AGCAGGCAAT ATCTGGAACT TCTCCAGTGG 720
CTTCTTCATT TCAGGGTATC AAAAAGTCTA TATTCAGAAT AAGAGAATCA CCTAAAGAGA 780
CTTTCAATGC AAGTTTTTCA GGTCAATATGA CTGATCCAAA CTTTAAAAAA GAAACTGAAG 840
CCTCTGAAAG TGGACTGGAA ATACATACTG TTTGCTCACA GAAGGAGGAC TCCTTATGTC 900
CAAATTTAAT TGATAATGGA AGCTGGCCAG CCACCACCAC ACAGAATTCT GTAGCTTTGA 960
AGAATGCAGG TTTAATATCC ACTTTGAAAA AGAAAACAAA TAAGTTTATT TATGCTATAC 1020
ATGATGAAAC ATTTTATAAA GGAAAAAAA TACCGAAAGA CCAAAAATCA GAACTAATTA 1080
ACTGTTTCAGC CCAGTTTGAA GCAAATGCTT TTGAAGCACC ACTTACATTT GCAAATGCTG 1140
ATTCAGGTAC CTCTGTCT 1158
```

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4987 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 1...4987
- (D) OTHER INFORMATION: Exon 11, nucleotides 20-4951 correspond to nucleotides 2138-7069 of complete coding sequence

(ix) FEATURE

(A) NAME/KEY: variable

(B) LOCATION: 339...1917

(D) OTHER INFORMATION: Y at positions 339 or 1917 = C or T;  
R at positions 790, 1081 or 1506 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```
TTTGTGTTTT TATGTTTAGG TTTATTGCAT TCTTCTGTGA AAAGAAGCTG TTCACAGAAT 60
GATTCTGAAG AACCAACTTT GTCCTTAACT AGCTCTTTTG GGACAATTCT GAGGAAATGT 120
TCTAGAAATG AAACATGTTC TAATAATACA GTAATCTCTC AGGATCTTGA TTATAAAGAA 180
GCAAAATGTA ATAAGGAAAA ACTACAGTTA TTTATTACCC CAGAAGCTGA TTCTCTGTCA 240
TGCCTGCAGG AAGGACAGTG TGAAAATGAT CCAAAAAGCA AAAAAGTTTC AGATATAAAA 300
GAAGAGGTCT TGGCTGCAGC ATGTCACCCA GTACAACAYT CAAAAGTGGA ATACAGTGAT 360
ACTGACTTTT AATCCCAGAA AAGTCTTTTA TATGATCATG AAAATGCCAG CACTCTTATT 420
TTAACTCCTA CTTCCAAGGA TGTTCGTGCA AACCTAGTCA TGATTTCTAG AGGCAAAGAA 480
TCATACAAAA TGTCAGACAA GCTCAAAGGT AACAAATTATG AATCTGATGT TGAATTAACC 540
AAAAATATTC CCATGGAAAA GAATCAAGAT GTATGTGCTT TAAATGAAAA TTATAAAAAC 600
GTTGAGCTGT TGCCACCTGA AAAATACATG AGAGTAGCAT CACCTTCAAG AAAGGTACAA 660
TTCAACCAAA ACACAAATCT AAGAGTAATC CAAAAAATC AAGAAGAAAC TACTTCAATT 720
TCAAAAATAA CTGTCAATCC AGACTCTGAA GAACTTTTCT CAGACAATGA GAATAATTTT 780
GTCTTCCAAR TAGCTAATGA AAGGAATAAT CTTGCTTTAG GAAATACTAA GGAACCTCAT 840
GAAACAGACT TGACTTGTGT AAACGAACCC ATTTTCAAGA ACTCTACCAT GGTTTTATAT 900
GGAGACACAG GTGATAAACA AGCAACCCAA GTGTCAATTA AAAAAGATTT GGTTTATGTT 960
CTTGACAGAG AGAACAAAAA TAGTGTAAG CAGCATATAA AAATGACTCT AGGTCAAGAT 1020
TTAAATCGG ACATCTCCTT GAATATAGAT AAAATACCAG AAAAAATAA TGATTACATG 1080
RACAAATGGG CAGGACTCTT AGGTCCAATT TCAAATCACA GTTTTGAGG TAGCTTCAGA 1140
ACAGCTTCAA ATAAGGAAAT CAAGCTCTCT GAACATAACA TTAAGAAGAG CAAAATGTTC 1200
TTCAAAGATA TTGAAGAACA ATATCCTACT AGTTTAGCTT GTGTTGAAAT TGTAATAACC 1260
TTGGCATTAG ATAATCAAAA GAAACTGAGC AAGCCTCAGT CAATTAATAC TGTATCTGCA 1320
CATTTACAGA GTAGTGTAGT TGTTTCTGAT TGTAATAATA GTCATATAAC CCTCAGATG 1380
TTATTTTCCA AGCAGGATTT TAATTCAAAC CATAATTTAA CACCTAGCCA AAAGGCAGAA 1440
ATTACAGAAC TTTCTACTAT ATTAGAAGAA TCAGGAAGTC AGTTTGAATT TACTCAGTTT 1500
AGAAARCCAA GCTACTAATT GCAGAAGAGT ACATTTGAAG TGCCTGAAAA CCAGATGACT 1560
ATCTTAAAGA CCACTTCTGA GGAATGCAGA GATGCTGATC TTCATGTCAT AATGAATGCC 1620
CCATCGATTG GTCAGGTAGA CAGCAGCAAG CAATTTGAAG GTACAGTTGA AATTAAACGG 1680
AAGTTTGCTG GCCTGTTGAA AAATGACTGT AACAAAAGTG CTTCTGGTTA TTAAACAGAT 1740
GAAAATGAAG TGGGGTTTAG GGGCTTTTAT TCTGCTCATG GCACAAAACCT GAATGTTTCT 1800
ACTGAAGCTC TGCAAAAAGC TGTGAACTG TTTAGTGATA TTGAGAATAT TAGTGAGGAA 1860
ACTTCTGCAG AGGTACATCC AATAAGTTTA TCTTCAAGTA AATGTCATGA TTCTGTYGTT 1920
TCAATGTTTA AGATAGAAAA TCATAATGAT AAAACTGTAA GTGAAAAAAA TAATAAATGC 1980
CAACTGATAT TACAAAATAA TATTGAAATG ACTACTGGCA CTTTTGTTGA AGAAATTACT 2040
GAAAATTACA AGAGAAATAC TGAAAATGAA GATAACAAAT ATACTGCTGC CAGTAGAAAT 2100
TCTCATAACT TAGAATTTGA TGGCAGTGAT TCAAGTAAAA ATGATACTGT TTGTATTTCAT 2160
AAAGATGAAA CGGACTTGCT ATTTACTGAT CAGCACAACA TATGTCTTAA ATTATCTGGC 2220
CAGTTTATGA AGGAGGGAAA CACTCAGATT AAAGAAGATT TGTCAGATTT AACTTTTTTTG 2280
GAAGTTGCGA AAGCTCAAGA AGCATGTCAT GGTAATACTT CAAATAAAGA ACAGTTAACT 2340
GCTACTAAAA CGGAGCAAAA TATAAAAGAT TTTGAGACTT CTGATACATT TTTTCAGACT 2400
GCAAGTGCGA AAAATATTAG TGTGCGCAAA GAGTCATTTA ATAAAATTGT AAATTTCTTT 2460
GATCAGAAAC CAGAAGAATT GCATAACTTT TCCTTAAATT CTGAATTACA TTCTGACATA 2520
AGAAAGAACA AAATGGACAT TCTAAGTTAT GAGGAAACAG ACATAGTTAA ACACAAAATA 2580
CTGAAAGAAA GTGTCCAGT TGGTACTGGA AATCAACTAG TGACCTTCCA GGGACAACCC 2640
GAACGTGATG AAAAGATCAA AGAACCTACT CTGTTGGGTT TTCATACAGC TAGCGGGAAA 2700
AAAGTTAAAA TTGCAAAGGA ATCTTTGGAC AAAGTGAAAA ACCTTTTTTGA TGAAAAAGAG 2760
CAAGGTACTA GTGAAATCAC CAGTTTTAGC CATCAATGGG CAAAGACCCT AAAGTACAGA 2820
GAGGCCTGTA AAGACCTTGA ATTAGCATGT GAGACCATTG AGATCACAGC TGCCCCAAAG 2880
```



TGTAAAGAAA	TGCAGAATTC	TCTCAATAAT	GATAAAAAACC	TTGTTTCTAT	TGAGACTGTG	2940
GTGCCACCTA	AGCTCTTAAG	TGATAATTTA	TGTAGACAAA	CTGAAAATCT	CAAAACATCA	3000
AAAAGTATCT	TTTTGAAAGT	TAAAGTACAT	GAAAATGTAG	AAAAAGAAAC	AGCAAAAAGT	3060
CCTGCAACTT	GTTACACAAA	TCAGTCCCCT	TATTCACTCA	TTGAAAATTC	AGCCTTAGCT	3120
TTTTACACAA	GTTGTAGTAG	AAAAACTTCT	GTGAGTCAGA	CTTCATTACT	TGAAGCAAAA	3180
AAATGGCTTA	GAGAAGGAAT	ATTTGATGGT	CAACCAGAAA	GAATAAATAC	TGCAGATTAT	3240
GTAGGAAATT	ATTTGTATGA	AAATAATTCA	AACAGTACTA	TAGCTGAAAA	TGACAAAAAT	3300
CATCTCTCCG	AAAAACAAGA	TACTTATTTA	AGTAACAGTA	GCATGTCTAA	CAGCTATTCC	3360
TACCATTCTG	ATGAGGTATA	TAATGATTCA	GGATATCTCT	CAAAAAATAA	ACTTGATTCT	3420
GGTATTGAGC	CAGTATTGAA	GAATGTTGAA	GATCAAAAAA	ACACTAGTTT	TTCCAAAGTA	3480
ATATCCAATG	TAAAAGATGC	AAATGCATAC	CCACAAACTG	TAAATGAAGA	TATTTGCGTT	3540
GAGGAACTTG	TGACTAGCTC	TTCACCCTGC	AAAAATAAAA	ATGCAGCCAT	TAAATTGTCC	3600
ATATCTAATA	GTAATAATTT	TGAGGTAGGG	CCACCTGCAT	TTAGGATAGC	CAGTGGTAA	3660
ATCGTTTGTG	TTTCACATGA	AACAATTAAA	AAAGTGAAAG	ACATATTTAC	AGACAGTTTC	3720
AGTAAAGTAA	TTAAGGAAAA	CAACGAGAAT	AAATCAAAAA	TTTGCCAAAC	GAAAATTATG	3780
GCAGGTTGTT	ACGAGGCATT	GGATGATTCA	GAGGATATTC	TTCATAACTC	TCTAGATAAT	3840
GATGAATGTA	GCACGCATT	ACATAAGGTT	TTTGCTGACA	TTCAGAGTGA	AGAAAATTTTA	3900
CAACATAACC	AAAAATATGTC	TGGATTGGAG	AAAGTTTCTA	AAATATCACC	TTGTGATGTT	3960
AGTTTGGAAA	CTTCAGATAT	ATGTAAATGT	AGTATAGGGA	AGCTTCATAA	GTCAGTCTCA	4020
TCTGCAATA	CTTGTGGGAT	TTTTAGCACA	GCAAGTGGAA	AATCTGTCCA	GGTATCAGAT	4080
GCTTCATTAC	AAAACGCAAG	ACAAGTGTTC	TCTGAAATAG	AAGATAGTAC	CAAGCAAGTC	4140
TTTTCCAAAG	TATTGTTTAA	AAGTAACGAA	CATTTCAGACC	AGCTCACAAG	AGAAGAAAAT	4200
ACTGCTATAC	GTACTCCAGA	ACATTTAATA	TCCCAAAAAG	GCTTTTCATA	TAATGTGGTA	4260
AATTCATCTG	CTTTCTCTGG	ATTTAGTACA	GCAAGTGGAA	AGCAAGTTTC	CATTTTAGAA	4320
AGTTCCTTAC	ACAAAGTTAA	GGGAGTGTTA	GAGGAATTTG	ATTTAATCAG	AACTGAGCAT	4380
AGTCTTCACT	ATTCACCTAC	GTCTAGACAA	AATGTATCAA	AAATACTTCC	TCGTGTTGAT	4440
AAGAGAAACC	CAGAGCACTG	TGTAAACTCA	GAAATGGAAA	AAACCTGCAG	TAAAGAATTT	4500
AAATTATCAA	ATAACTTAAA	TGTTGAAGGT	GGTTCTTCAG	AAAATAATCA	CTCTATTAAA	4560
GTTTCTCCAT	ATCTCTCTCA	ATTTCAACAA	GACAAACAAC	AGTTGGTATT	AGGAACCAAA	4620
GTCTCACTTG	TTGAGAACAT	TCATGTTTTG	GGAAAAGAAC	AGGCTTCACC	TAAAAACGTA	4680
AAAAATGGAAA	TTGGTAAAC	TGAAACTTTT	TCTGATGTTT	CTGTGAAAAC	AAATATAGAA	4740
GTTTGTCTTA	CTTACTCCAA	AGATTTCAGAA	AACTACTTTG	AAACAGAAGC	AGTAGAAAAT	4800
GCTAAAGCTT	TTATGGAAGA	TGATGAACGT	ACAGATTCTA	AACTGCCAAG	TCATGCCACA	4860
CATTCTCTTT	TTACATGTCC	CGAAAATGAG	GAAATGGTTT	TGTCAAATTC	AAGAATTGGA	4920
AAAAGAAGAG	GAGAGCCCCCT	TATCTTAGTG	GGTAAGTGTT	CATTTTTTACC	TTTCGTGTTG	4980
CCAATCA						4987

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 1...468
- (D) OTHER INFORMATION: Exon 14, nucleotides 12-439 correspond to nucleotides 7236-7663 of complete coding sequence

(ix) FEATURE

- (A) NAME/KEY: variable
- (B) LOCATION: 248
- (D) OTHER INFORMATION: R at position 248 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```
CCCCATTGCA GCACAACCTAA GGAACGTCAA GAGATACAGA ATCCAAATTT TACCGCACCT 60
GGTCAAGAAT TTCTGTCTAA ATCTCATTTG TATGAACATC TGACTTTGGA AAAATCTTCA 120
AGCAATTTAG CAGTTTCAGG ACATCCATTT TATCAAGTTT CTGCTACAAG AAATGAAAAA 180
ATGAGACACT TGATTACTAC AGGCAGACCA ACCAAAGTCT TTGTTCCACC TTTTAAAACT 240
AAATCACRTT TTCACAGAGT TGAACAGTGT GTTAGGAATA TTAAGTTGGA GGAAAAACAGA 300
CAAAAGCAAA ACATTGATGG ACATGGCTCT GATGATAGTA AAAATAAGAT TAATGACAAT 360
GAGATTCATC AGTTTAAACA AAACAACCTCC AATCAAGCAG CAGCTGTAAC TTTCACAAAG 420
TGTGAAGAAG AACCTTTAGG TATTGTATGA CAATTTGTGT GATGAATT 468
```

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 1...255
- (D) OTHER INFORMATION: Exon 22, nucleotides 31-229 correspond to nucleotides 8983-9181 of complete coding sequence

(ix) FEATURE

- (A) NAME/KEY: variable
- (B) LOCATION: 127
- (D) OTHER INFORMATION: R at position 127 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```
TTTTTATTCC AATATCTTAA ATGGTCACAG GGTTATTTCA GTGAAGAGCA GTTAAGAGCC 60
TTGAATAATC ACAGGCAAAT GTTGAATGAT AAGAAACAAG CTCAGATCCA GTTGGAAATT 120
AGGAAGRCCA TGGAATCTGC TGAACAAAAG GAACAAGGTT TATCAAGGGA TGTCACAACC 180
GTGTGGAAGT TCGTATTGT AAGCTATTCA AAAAAAGAAA AAGATTCAGG TAAGTATGTA 240
AATGCTTTGT TTTTA 255
```

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 31...135
- (D) OTHER INFORMATION: Exon 2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```
TAAGTGCATT TTGGTCTTCT GTTTTCAGCA CTTATTTACC AAGCATTGGA GGAATATCGT 60
AGGTAAAAAT GCCTATTGGA TCCAAAGAGA GGCCAACATT TTTTGAAATT TTTAAGACAC 120
```

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 21...269
- (D) OTHER INFORMATION: Exon 3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```
GGGATTTTTT TTTTAAATAG ATTTAGGACC AATAAGTCTT AATTGGTTTG AAGAACTTTC 60
TTCAGAAGCT CCACCCTATA ATTCTGAACC TGCAGAAGAA TCTGAACATA AAAACAACAA 120
TTACGAACCA AACCTATTTA AAACCTCCACA AAGGAAACCA TCTTATAATC AGCTGGCTTC 180
AACTCCAATA ATATTCAAAG AGCAAGGGCT GACTCTGCCG CTGTACCAAT CTCCTGTAAA 240
AGAATTAGAT AAATTCAAAT TAGACTTAGG TAAGTAATGC AATATGGTAG ACTGGGG 297
```

## (2) INFORMATION FOR SEQ ID NO:117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 26...134
- (D) OTHER INFORMATION: Exon 4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```
TCACTGAATT ATTGTACTGT TTCAGGAAGG AATGTTCCCA ATAGTAGACA TAAAAGTCTT 60
CGCACAGTGA AACTTAAAT GGATCAAGCA GATGATGTTT CCTGTCCACT TCTAAATTCT 120
TGTCTTAGTG AAAGGTATGA TGAAGCTATT ATATTAAAA 159
```

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 31...71
- (D) OTHER INFORMATION: Exon 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```
TTAACAATTT TCCCCTTTTT TTACCCCCAG TGGTATGTGG GAGTTTGTTC CATAACCAA 60
AGTTTGTGAA GGTAAATATT                                     80
```

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 51...165
- (D) OTHER INFORMATION: Exon 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```
TAATGATCAG GGCATTTCTA TAAAAAATAA ACTATTTTCT TTCCTCCCAG GGTCGTCAGA 60
CACCAAAACA TATTTCTGAA AGTCTAGGAG CTGAGGTGGA TCCTGATATG TCTTGGTCAA 120
GTTCTTTAGC TACACCACCC ACCCTTAGTT CTACTGTGCT CATAGGTAAT AATA       174
```

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 14...63
- (D) OTHER INFORMATION: Exon 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```
TTTTATCTTA CAGTCAGAAA TGAAGAAGCA TCTGAAACTG TATTTCTCTA TGATACTACT 60
GCTGTAAAGTA AATATGACAT TGATTAGACT                                     90
```

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 20...131

(D) OTHER INFORMATION: Exon 9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```
TAAACTATAA TTTTTCGAGA ATGTGAAAAG CTATTTTTC AATCATGATG AAAGTCTGAA 60
GAAAAATGAT AGATTTATCG CTTCTGTGAC AGACAGTGAA AACACAAATC AAAGAGAAGC 120
TGCAAGTCAT GGTAAGTCCT CT 142
```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 29...124
- (D) OTHER INFORMATION: Exon 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
AAAACATATA TGAAATATTT CTTTTTAGGA GAACCCTCAA TCAAAAGAAA CTTATTAAAT 60
GAATTTGACA GGATAATAGA AAATCAAGAA AAATCCTTAA AGGCTTCAAA AAGCACTCCA 120
GATGGTAAAA TTAGCTTTTT ATTTATA 147
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 31...100
- (D) OTHER INFORMATION: Exon 13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

```
AATATGTAAT ATAAAATAAT TGTTTCCTAG GCACAATAAA AGATCGAAGA TTGTTTATGC 60
ATCATGTTTC TTTAGAGCCG ATTACCTGTG TACCCTTTTC GTAAGACATG TTTAAATTTT 120
TCTAA 125
```

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 13...183

(D) OTHER INFORMATION: Exon 17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

```
TTATTTGTTT AGGGCTCTGT GTGACACTCC AGGTGTGGAT CCAAAGCTTA TTTCTAGAAT 60
TTGGGTTTTT AATCACTATA GATGGATCAT ATGGAAACTG GCAGCTATGG AATGTGCCTT 120
TCCTAAGGAA TTTGCTAATA GATGCCTAAG CCCAGAAAGG GTGCTTCTTC AACTAAAATA 180
CAGGCAAGTT TAAAGCATT                                     199
```

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 19...373

(D) OTHER INFORMATION: Exon 18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```
TTTTGTTTTT ACTTTTAGAT ATGATACGGA AATTGATAGA AGCAGAAGAT CGGCTATAAA 60
AAAGATAATG GAAAGGGATG ACACAGCTGC AAAAACACTT GTTCTCTGTG TTTCTGACAT 120
AATTTTCATT AGCGCAAATA TATCTGAAAC TTCTAGCAAT AAAACTAGTA GTGCAGATAC 180
CCAAAAAGTG GCCATTATTG AACTTACAGA TGGGTGGTAT GCTGTTAAGG CCCAGTTAGA 240
TCCTCCCCTC TTAGCTGTCT TAAAGAATGG CAGACTGACA GTTGGTCAGA AGATTATTCT 300
TCATGGAGCA GAACTGGTGG GCTCTCCTGA TGCCTGTACA CCTCTTGAAG CCCCAGAATC 360
TCTTATGTTA AAGGTAAATT                                     380
```

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 30...185

(D) OTHER INFORMATION: Exon 19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```
TAAATCAATA TATTTATTAA TTTGTCCAGA TTTCTGCTAA CAGTACTCGG CCTGCTCGCT 60
GGTATACCAA ACTTGGATTC TTTCTGACC CTAGACCTTT TCCTCTGCCC TTATCATCGC 120
TTTTCACTGA TGGAGGAAAT GTTGGTTGTG TTGATGTAAT TATTCAAAGA GCATACCCTA 180
TACAGGTATG ATGTATTCTT GAAACTTA                                     208
```

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 28...172
- (D) OTHER INFORMATION: Exon 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```
TTTGGTGTGT GTAACACATT ATTACAGTGG ATGGAGAAGA CATCATCTGG ATTATACATA 60
TTTCGCAATG AAAGAGAGGA AGAAAAGGAA GCAGCAAAAT ATGTGGAGGC CCAACAAAAG 120
AGACTAGAAG CCTTATTCAC TAAAATTCAG GAGGAATTG AAGAACATGA AGGTAAATTT 180
AGTTATATGG TACACATTGT TATTTT                                     206
```

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 36...157
- (D) OTHER INFORMATION: Exon 21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```
AGTTTAGTGA ATTAATAATC CTTTGTGTTT CTTAGAAAAC ACAACAAAAC CATATTTACC 60
ATCACGTGCA CTAACAAGAC AGCAAGTTCG TGCTTTGCAA GATGGTGCAG AGCTTTATGA 120
AGCAGTGAAG AATGCAGCAG ACCCAGCTTA CCTTGAGGTG AGAGAGTAAG AGGACATATA 180
ATGAG                                             185
```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 12...175
- (D) OTHER INFORMATION: Exon 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
TCTCCAAACA GTTATACTGA GTATTTGGCG TCCATCATCA GATTTATATT CTCTGTTAAC 60
AGAAGGAAAG AGATACAGAA TTTATCATCT TGCAACTTCA AAATCTAAAA GTAAATCTGA 120
AAGAGCTAAC ATACAGTTAG CAGCGACAAA AAAA ACTCAG TATCAACAAC TACCGGTACA 180
AACCTTTCAT TGTAATTTTTT                                     200
```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 25...163
- (D) OTHER INFORMATION: Exon 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```
GAATTTTGT TTTGTTTCT GTAGGTTTCA GATGAAATTT TATTTTCAGAT TTACCAGCCA 60
CGGGAGCCCC TTCACTTCAG CAAATTTTGA GATCCAGACT TTCAGCCATC TTGTTCTGAG 120
GTGGACCTAA TAGGATTTGT CGTTTCTGTT GTGAAAAAAA CAGGTAATGC ACAATATAGT 180
TAATTTTTTTT TATTGATTCT TTTAAAAAAC ATTGTTCT                                     217
```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 31...275
- (D) OTHER INFORMATION: Exon 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
TAACATTCTT TTCTTTTTTT TCCATTCTAG GACTTGCCCC TTTCGTCTAT TTGTCAGACG 60
AATGTTACAA TTTACTGGCA ATAAAGTTTT GGATAGACCT TAATGAGGAC ATTATTAAGC 120
CTCATATGTT AATTGCTGCA AGCAACCTCC AGTGGCGACC AGAATCCAAA TCAGGCCTTC 180
TTACTTTATT TGCTGGAGAT TTTTCTGTGT TTTCTGCTAG TCCAAAAGAG GGCCACTTTC 240
AAGAGACATT CAACAAAATG AAAAATACTG TTGAGGTAAG GTTA                                     284
```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE  
     (A) NAME/KEY: exon  
     (B) LOCATION: 31...177  
     (D) OTHER INFORMATION: Exon 26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
ATAAAGCAGC TTTTCCACTT ATTTTCTTAG AATATTGACA TACTTTGCAA TGAAGCAGAA 60
ACAAGCTTA TGCATATACT GCATGCAAAT GATCCCAAGT GGTCCACCCC AACTAAAGAC 120
TGTAATTCTAG GGCCGTACAC TGCTCAAATC ATTCTTGGTA CAGGAAACAA GCTTCTGGTA 180
AGTTAATGTA AACTCAAGGA ATATTATAAG                210
```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 691 base pairs  
     (B) TYPE: nucleic acid  
     (C) STRANDEDNESS: single  
     (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE  
     (A) NAME/KEY: exon  
     (B) LOCATION: 23...691  
     (D) OTHER INFORMATION: Exon 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```
TACGTTTTCA TTTTTTTATC AGATGTCTTC TCCTAATTGT GAGATATATT ATCAAAGTCC 60
TTTATCACTT TGTATGGCCA AAAGGAAGTC TGTTTCCACA CCTGTCTCAG CCCAGATGAC 120
TTCAAAGTCT TGTAAGGGG AGAAAGAGAT TGATGACCAA AAGAACTGCA AAAAGAGAAG 180
AGCCTTGGAT TTCTTGAGTA GACTGCCTTT ACCTCCACCT GTTAGTCCCA TTTGTACATT 240
TGTTTCTCCG GCTGCACAGA AGGCATTTCA GCCACCAAGG AGTTGTGGCA CCAAATACGA 300
AACACCCATA AAGAAAAAAG AACTGAATTC TCCTCAGATG ACTCCATTTA AAAAATTCAA 360
TGAAATTTCT CTTTTGGAAA GTAATTCAAT AGCTGACGAA GAACTTGCAT TGATAAATAC 420
CCAAGCTCTT TTGTCTGGTT CAACAGGAGA AAAACAATTT ATATCTGTCA GTGAATCCAC 480
TAGGACTGCT CCCACCAGTT CAGAAGATTA TCTCAGACTG AAACGACGTT GTACTACATC 540
TCTGATCAAA GAACAGGAGA GTTCCCAGGC CAGTACGGAA GAATGTGAGA AAAATAAGCA 600
GGACACAATT ACAACTAAAA AATATATCTA AGCATTGCA AAGGCGACAA TAAATTATTG 660
ACGCTTAACC TTTCCAGTTT ATAAGACTGG A                691
```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 10987 base pairs  
     (B) TYPE: nucleic acid  
     (C) STRANDEDNESS: single  
     (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE  
     (A) NAME/KEY: coding sequence  
     (B) LOCATION: 229...10485  
     (D) OTHER INFORMATION: GenBank Accession No. U43746, BRCA2 gene

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GGTGGCGCGA	GCTTCTGAAA	CTAGGCGGCA	GAGGCGGAGC	CGCTGTGGCA	CTGCTGCGCC	60
TCTGCTGCGC	CTCGGGTGTG	TTTTGCGGCG	GTGGGTCGCC	GCCGGGAGAA	GCGTGAGGGG	120
ACAGATTTGT	GACCGGCGCG	GTTTTTGTCA	GCTTACTCCG	GCCAAAAAAG	AACTGCACCT	180
CTGGAGCGGA	CTTATTTACC	AAGCATTGGA	GGAATATCGT	AGGTAAAAAT	GCCTATTGGA	240
TCCAAAGAGA	GGCCAACATT	TTTTGAAATT	TTAAGACAC	GCTGCAACAA	AGCAGATTTA	300
GGACCAATAA	GTCTTAATTG	GTTTGAAGAA	CTTCTTCAG	AAGCTCCACC	CTATAATTCT	360
GAACCTGCAG	AAGAATCTGA	ACATAAAAAAC	AACAATTACG	AACCAAACCT	ATTTAAAACT	420
CCACAAAGGA	AACCATCTTA	TAATCAGCTG	GCTTCAACTC	CAATAATATT	CAAAGAGCAA	480
GGGCTGACTC	TGCCGCTGTA	CCAATCTCCT	GTAAAAAGAA	TAGATAAATT	CAAATTAGAC	540
TTAGGAAGGA	ATGTTCCCAA	TAGTAGACAT	AAAAGTCTTC	GCACAGTGAA	AACTAAAATG	600
GATCAAGCAG	ATGATGTTTC	CTGTCCACTT	CTAAATCTTT	GTCTTAGTGA	AAGTCCTGTT	660
GTTCTACAAT	GTACACATGT	AACACCACAA	AGAGATAAGT	CAGTGGTATG	TGGGAGTTTG	720
TTTCATACAC	CAAAGTTTGT	GAAGGGTCGT	CAGACACCAA	AACATATTTC	TGAAAGTCTA	780
GGAGCTGAGG	TGGATCCTGA	TATGTCTTGG	TCAAGTCTTT	TAGCTACACC	ACCCACCCCTT	840
AGTTCTACTG	TGCTCATAGT	CAGAAATGAA	GAAGCATCTG	AAACTGTATT	TCCTCATGAT	900
ACTACTGCTA	ATGTGAAAAG	CTATTTTTTC	AATCATGATG	AAAGTCTGAA	GAAAAATGAT	960
AGATTTATCG	CTTCTGTGAC	AGACAGTGAA	AACACAAATC	AAAGAGAAGC	TGCAAGTCAT	1020
GGATTTGGAA	AAACATCAGG	GAATTCATTT	AAAGTAAATA	GCTGCAAAGA	CCACATTGGA	1080
AAGTCAATGC	CAAATGTCCT	AGAAGATGAA	GTATATGAAA	CAGTTGTAGA	TACCTCTGAA	1140
GAAGATAGTT	TTTCATTATG	TTTTTCTAAA	TGTAGAACAA	AAAATCTACA	AAAAGTAAGA	1200
ACTAGCAAGA	CTAGGAAAAA	AATTTTCCAT	GAAGCAAACG	CTGATGAATG	TGAAAAATCT	1260
AAAAACCAAG	TGAAAGAAAA	ATACTCATTT	GTATCTGAAG	TGGAACCAAA	TGATACTGAT	1320
CCATTAGATT	CAAATGTAGC	ACATCAGAAG	CCCTTTGAGA	GTGGAAGTGA	CAAAATCTCC	1380
AAGGAAGTTG	TACCGTCTTT	GGCCTGTGAA	TGGTCTCAAC	TAACCCCTTC	AGGTCTAAAT	1440
GGAGCCGAGA	TGGAGAAAAT	ACCCCTATTG	CATATTTCTT	CATGTGACCA	AAATATTTCA	1500
GAAAAAGACC	TATTAGACAC	AGAGAACAAA	AGAAAGAAAG	ATTTTCTTAC	TTCAGAGAAT	1560
TCTTTGCCAC	GTATTTCTAG	CCTACCAAAA	TCAGAGAAGC	CATTAAATGA	GGAAACAGTG	1620
GTAAATAAGA	GAGATGAAGA	GCAGCATCTT	GAATCTCATA	CAGACTGCAT	TCTTGCACTA	1680
AAGCAGGCAA	TATCTGGAAC	TTCTCCAGTG	GCTTCTTCAT	TTCAGGGTAT	CAAAAAGTCT	1740
ATATTAGAAA	TAAGAGAATC	ACCTAAAGAG	ACTTTCAATG	CAAGTTTTTC	AGGTCATATG	1800
ACTGATCCAA	ACTTTAAAAA	AGAAACTGAA	GCCTCTGAAA	GTGGACTGGA	AATACATACT	1860
GTTTGCTCAC	AGAAGGAGGA	CTCCTTATGT	CCAAATTTAA	TTGATAATGG	AAGCTGGCCA	1920
GCCACCACCA	CACAGAATTC	TGTAGCTTTG	AAGAATGCAG	GTTTAATATC	CACTTTGAAA	1980
AAGAAAACAA	ATAAGTTTAT	TTATGCTATA	CATGATGAAA	CATTTTATAA	AGGAAAAAAA	2040
ATACCGAAAG	ACCAAAAATC	AGAATAAATT	AACTGTTTCA	CCCAGTTTGA	AGCAAAATGCT	2100
TTTGAAGCAC	CACTTACATT	TGCAAAATGCT	GATTCAGGTT	TATTGCATTG	TTCTGTGAAA	2160
AGAAGCTGTT	CACAGAATGA	TTCTGAAGAA	CCAACTTTGT	CCTTAACTAG	CTCTTTTGGG	2220
ACAATTCTGA	GGAAATGTTT	TAGAAATGAA	ACATGTTCTA	ATAATACAGT	AATCTCTCAG	2280
GATCTTGATT	ATAAAGAAGC	AAAATGTAAT	AAGGAAAAAC	TACAGTTATT	TATTACCCCA	2340
GAAGCTGATT	CTCTGTCATG	CCTGCAGGAA	GGACAGTGTG	AAAATGATCC	AAAAAGCAAA	2400
AAAGTTTCAG	ATATAAAAGA	AGAGGTCTTG	GCTGCAGCAT	GTCACCCAGT	ACAACATTCA	2460
AAAGTGGAAT	ACAGTGATAC	TGACTTTCAA	TCCCAGAAAA	GTCTTTTATA	TGATCATGAA	2520
AATGCCAGCA	CTCTTATTTT	AACTCCTACT	TCCAAGGATG	TTCTGTCAAA	CCTAGTCATG	2580
ATTTCTAGAG	GCAAGAATC	ATACAAAATG	TCAGACAAGC	TCAAAGGTAA	CAATTATGAA	2640
TCTGATGTTG	AATTAACCAA	AAATATTCCC	ATGGAAAAGA	ATCAAGATGT	ATGTGCTTTA	2700
AATGAAAAAT	ATAAAAAACG	TGAGCTGTTG	CCACCTGAAA	AATACATGAG	AGTAGCATCA	2760
CCTTCAAGAA	AGGTACAATT	CAACCAAAAC	ACAAATCTAA	GAGTAATCCA	AAAAATCAA	2820
GAAGAACTA	CTTCAATTTT	AAAAATAACT	GTCAATCCAG	ACTCTGAAGA	ACTTTTCTCA	2880
GACAATGAGA	ATAATTTTGT	CTTCCAAGTA	GCTAATGAAA	GGAATAATCT	TGCTTTAGGA	2940
AATACTAAGG	AACTTCATGA	AACAGACTTG	ACTTGTGTAA	ACGAACCCAT	TTTCAAGAAC	3000
TCTACCATGG	TTTATATGGG	AGACACAGGT	GATAAACAAG	CAACCCAGT	GTCAATTAAA	3060
AAAGATTTGG	TTTATGTTCT	TGCAGAGGAG	AACAAAAATA	GTGTAAAGCA	GCATATAAAA	3120
ATGACTCTAG	GTCAAGATTT	AAAATCGGAC	ATCTCCTTGA	ATATAGATAA	AATACCAGAA	3180
AAAAATAATG	ATTACATGAA	CAAAATGGGCA	GGACTCTTAG	GTCCAATTTT	AAATCACAGT	3240
TTTGGAGGTA	GCTTCAGAAC	AGCTTCAAAT	AAGGAAATCA	AGCTCTCTGA	ACATAACATT	3300

AAGAAGAGCA	AAATGTTCTT	CAAAGATATT	GAAGAACAAT	ATCCTACTAG	TTTAGCTTGT	3360
GTTGAAATTG	TAAATACCTT	GGCATTAGAT	AATCAAAAGA	AACTGAGCAA	GCCTCAGTCA	3420
ATTAATACTG	TATCTGCACA	TTTACAGAGT	AGTGTAGTTG	TTTCTGATTG	TAAAAATAGT	3480
CATATAACCC	CTCAGATGTT	ATTTTCCAAG	CAGGATTTTA	ATTCAAACCA	TAATTTAACA	3540
CCTAGCCAAA	AGGCAGAAAT	TACAGAACTT	TCTACTATAT	TAGAAGAATC	AGGAAGTCAG	3600
TTTGAATTTA	CTCAGTTTAT	AAAACCAAGC	TACATATTGC	AGAAGAGTAC	ATTTGAAGTG	3660
CCTGAAAACC	AGATGACTAT	CTTAAAGACC	ACTTCTGAGG	AATGCAGAGA	TGCTGATCTT	3720
CATGTCATAA	TGAATGCCCC	ATCGATTGGT	CAGGTAGACA	GCAGCAAGCA	ATTTGAAGGT	3780
ACAGTTGAAA	TTAAACGGAA	GTTTGCTGGC	CTGTTGAAAA	ATGACTGTAA	CAAAAGTGCT	3840
TCTGGTTATT	TAACAGATGA	AAATGAAGTG	GGGTTTAGGG	GCTTTTATTC	TGCTCATGGC	3900
ACAAAACCTGA	ATGTTTCTAC	TGAAGCTCTG	CAAAAAGCTG	TGAAACTGTT	TAGTGATATT	3960
GAGAATATTA	GTGAGGAAAC	TTCTGCAGAG	GTACATCCAA	TAAGTTTATC	TTCAAGTAAA	4020
TGTCATGATT	CTGTTGTTTC	AATGTTTAAG	ATAGAAAAATC	ATAATGATAA	AACTGTAAAGT	4080
GAAAAAATA	ATAAATGCCA	ACTGATATTA	CAAAAATAAT	TTGAAATGAC	TACTGGCACT	4140
TTTGTGGAAG	AAATTACTGA	AAATTACAAG	AGAAATACCTG	AAAATGAAGA	TAACAAATAT	4200
ACTGCTGCCA	GAATAAATTC	TCATAACTTA	GAATTTGATG	GCAGTGATTTC	AAGTAAAAAT	4260
GATACTGTTT	GTATTCATAA	AGATGAAACG	GACTTGCTAT	TTACTGATCA	GCACAACATA	4320
TGTCTTAAAT	TATCTGGCCA	GTTTATGAAG	GAGGGAAACA	CTCAGATTAA	AGAAGATTTG	4380
TCAGATTTAA	CTTTTTTGGG	AGTTGCGAAA	GCTCAAGAAG	CATGTCATGG	TAATACTTCA	4440
AATAAAGAAC	AGTTAACTGC	TACTAAAACG	GAGCAAAATA	TAAAAGATTT	TGAGACTTCT	4500
GATACATTTT	TTCAGACTGC	AAGTGGGAAA	AATATTAGTG	TCGCCAAAGA	GTCAATTTAAT	4560
AAAATTGTAA	ATTTCTTTGA	TCAGAAACCA	GAAGAATTGC	ATAACTTTTC	CTTAAATTCT	4620
GAATTACATT	CTGACATAAG	AAAGAACAAA	ATGGACATTC	TAAGTTATGA	GGAAACAGAC	4680
ATAGTTAAAC	ACAAAATACT	GAAAGAAAGT	GTCCCAGTTG	GTACTGGAAA	TCAACTAGTG	4740
ACCTTCCAGG	GACAACCCGA	ACGTGATGAA	AAGATCAAAG	AACCTACTCT	GTTGGGTTTT	4800
CATACAGCTA	GCGGGAAAAA	AGTTAAAATT	GCAAAGGAAT	CTTTGGACAA	AGTGAAAAAC	4860
CTTTTGTATG	AAAAAGAGCA	AGGTACTAGT	GAAATCACCA	GTTTTAGCCA	TCAATGGGCA	4920
AAGACCCTAA	AGTACAGAGA	GGCCTGTAAA	GACCTTGAAT	TAGCATGTGA	GACCATTGAG	4980
ATCACAGCTG	CCCCAAAGTG	TAAAGAAATG	CAGAATTCTC	TCAATAATGA	TAAAAACCTT	5040
GTTTCTATTG	AGACTGTGGT	GCCACCTAAG	CTCTTAAGTG	ATAATTTATG	TAGACAAACT	5100
GAAAAATCTCA	AAACATCAAA	AAGTATCTTT	TTGAAAGTTA	AAGTACATGA	AAATGTAGAA	5160
AAAGAAACAG	CAAAAAGTCC	TGCAACTTGT	TACACAAATC	AGTCCCCTTA	TTCAAGTCATT	5220
GAAAAATTCAG	CCTTAGCTTT	TTACACAAGT	TGTATAGAAA	AAACTTCTGT	GAGTCAGACT	5280
TCATTACTTG	AAGCAAAAAA	ATGGCTTAGA	TAGAGGAATAT	TTGATGGTCA	ACCAGAAAAG	5340
ATAAACTACTG	CAGATAATGT	AGGAAATTAT	TTGTATGAAA	ATAATTCAAA	CAGTACTATA	5400
GCTGAAAAATG	ACAAAAATCA	TCTCTCCGAA	AAACAAGATA	CTTATTTAAG	TAACAGTAGC	5460
ATGTCTAACA	GCTATTCCTA	CCATTCTGAT	GAGGTATATA	ATGATTCAGG	ATATCTCTCA	5520
AAAAATAAAC	TTGATTCTGG	TATTGAGCCA	GTATTGAAGA	ATGTTGAAGA	TCAAAAAAAC	5580
ACTAGTTTTT	CCAAAGTAAT	ATCCAATGTA	AAAGATGCAA	ATGCATACCC	ACAAACTGTA	5640
AATGAAGATA	TTTGCGTTGA	GGAACCTGTG	ACTAGCTCTT	CACCCGTGCA	AAATAAAAAAT	5700
GCAGCCATTA	AATTGTCCAT	ATCTAATAGT	AATAATTTTG	AGGTAGGGCC	ACCTGCATTT	5760
AGGATAGCCA	GTGGTAAAAAT	CGTTTGTGTT	TCACATGAAA	CAATTAAAAA	AGTGAAAGAC	5820
ATATTTACAG	ACAGTTTCAG	TAAAGTAATT	AAGGAAAACA	ACGAGAATAA	ATCAAAAAAT	5880
TGCCAAACGA	AAATTATGGC	AGGTGTGTAC	GAGGCATTGG	ATGATTCAGA	GGATATTCTT	5940
CATAACTCTC	TAGATAATGA	TGAATGTAGC	ACGCATTAC	ATAAGGTTTT	TGCTGACATT	6000
CAGAGTGAAG	AAATTTTACA	ACATAACCAA	AATATGTCTG	GATTGGAGAA	AGTTTCTAAA	6060
ATATCACCTT	GTGATGTTAG	TTTGAAAAC	TCAGATATAT	GTAAATGTAG	TATAGGGAAG	6120
CTTCATAAGT	CAGTCTCATC	TGCAATAACT	TGTGGGATTT	TTAGCACAGC	AAGTGGAAAA	6180
TCTGTCCAGG	TATCAGATGC	TTCAATACAA	AACGCAAGAC	AAGTGTTTTC	TGAAATAGAA	6240
GATAGTACCA	AGCAAGTCTT	TTCCAAAGTA	TTGTTTAAAA	GTAACGAACA	TTCAAGACCAG	6300
CTCACAAGAG	AAGAAAAATAC	TGCTATACGT	ACTCCGAAC	ATTTAATATC	CCAAAAAGGC	6360
TTTTCATATA	ATGTGGTAAA	TTCATCTGCT	TTCTCTGGAT	TTAGTACAGC	AAGTGGAAAG	6420
CAAGTTTCCCA	TTTTAGAAAAG	TTCTTACAC	AAAGTTAAGG	GAGTGTTAGA	GGAATTTGAT	6480
TTAATCAGAA	CTGAGCATAG	TCTTCACTAT	TCACCTACGT	CTAGACAAAA	TGTATCAAAA	6540
ATACTTCCTC	GTGTTGATAA	GAGAAACCCA	GAGCACTGTG	TAAACTCAGA	AATGGAAAAA	6600
ACCTGCAGTA	AAGAATTTAA	ATTATCAAAT	AACTTAAATG	TTGAAGGTGG	TTCTTCAGAA	6660
AATAATCACT	CTATTAAAGT	TTCTCCATAT	CTCTCTCAAT	TTCAACAAGA	CAAACAACAG	6720

TTGGTATTAG	GAACCAAAGT	CTCACTTGTT	GAGAACATTC	ATGTTTTGGG	AAAAGAACAG	6780
GCTTCACCTA	AAAACGTAAA	AATGGAAAT	GGTAAAACTG	AAACTTTTTTC	TGATGTTCCCT	6840
GTGAAAACAA	ATATAGAAGT	TTGTTCTACT	TACTCCAAAG	ATTCAGAAAA	CTACTTTGAA	6900
ACAGAAGCAG	TAGAAATTGC	TAAAGCTTTT	ATGGAAGATG	ATGAACTGAC	AGATTCTAAA	6960
CTGCCAAGTC	ATGCCACACA	TTCTCTTTTT	ACATGTCCCG	AAAATGAGGA	AATGGTTTTG	7020
TCAAATTCAA	GAATTGGAAA	AAGAAGAGGA	GAGCCCCCTA	TCTTAGTGGG	AGAACCCTCA	7080
ATCAAAAGAA	ACTTATTTAA	TGAATTTGAC	AGGATAATAG	AAAAATCAAGA	AAAAATCCTTA	7140
AAGGCTTCAA	AAAGCACTCC	AGATGGCACA	ATAAAAGATC	GAAGATTGTT	TATGCATCAT	7200
GTTTCTTTAG	AGCCGATTAC	CTGTGTACCC	TTTCGCACAA	CTAAGGAACG	TCAAGAGATA	7260
CAGAAATCCAA	ATTTTACCGC	ACCTGGTCAA	GAATTTCTGT	CTAAATCTCA	TTTGTATGAA	7320
CATCTGACTT	TGGAAAAATC	TTCAAGCAAT	TTAGCAGTTT	CAGGACATCC	ATTTTATCAA	7380
GTTTCTGCTA	CAAGAAATGA	AAAAATGAGA	CACCTTGATTA	CTACAGGCAG	ACCAACCAAA	7440
GTCTTTGTTT	CACCTTTTAA	AACTAAATCA	CATTTTCACA	GAGTTGAACA	GTGTGTTAGG	7500
AATATTAAC	TGGAGGAAAA	CAGACAAAA	CAAAACATTG	ATGGACATGG	CTCTGATGAT	7560
AGTAAAAATA	AGATTTAATGA	CAATGAGATT	CATCAGTTTA	ACAAAAACAA	CTCCAATCAA	7620
GCAGCAGCTG	TAACTTTTAC	AAAGTGTGAA	GAAGAACCCT	TAGATTTAAT	TACAAGTCTT	7680
CAGAATGCCA	GAGATATACA	GGATATGCGA	ATTAAGAAGA	AACAAAAGGCA	ACGCGTCTTT	7740
CCACAGCCAG	GCAGTCTGTA	TCTTGCAAAA	ACATCCACTC	TGCCTCGAAT	CTCTCTGAAA	7800
GCAGCAGTAG	GAGGCCAAGT	TCCCTCTGCG	TGTTCTCATA	AACAGCTGTA	TACGTATGGC	7860
GTTTCTAAAC	ATTGCATAAA	AATTAACAGC	AAAAATGCAG	AGTCTTTTCA	GTTTCACACT	7920
GAAGATTATT	TTGGTAAGGA	AAGTTTATGG	ACTGGAAAAG	GAATACAGTT	GGCTGATGGT	7980
GGATGGCTCA	TACCTTCCAA	TGATGGAAAG	GCTGGAAAAG	AAGAATTTTA	TAGGGCTCTG	8040
TGTGACACTC	CAGGTGTGGA	TCCAAAGCTT	ATTTCTAGAA	TTTGGGTTTA	TAATCACTAT	8100
AGATGGATCA	TATGGAAACT	GGCAGCTATG	GAATGTGCCT	TTCCTAAGGA	ATTTGCTAAT	8460
AGATGCCATA	GCCCAGAAAG	GGTGCTTCTT	CAACTAAAAAT	ACAGATATGA	TACGGAAATT	8220
GATAGAAGCA	GAAGATCGGC	TATAAAAAAG	ATAATGGAAG	GGGATGACAC	AGCTGCAAAA	8280
ACACTTGTTT	TCTGTGTTTC	TGACATAATT	TCATTGAGCG	CAAATATATC	TGAAACTTCT	8340
AGCAATAAAA	CTAGTAGTGC	AGATACCCAA	AAAGTGGCCA	TTATTGAACT	TACAGATGGG	8400
TGGTATGCTG	TAAAGGCCCA	GTTAGATCCT	CCCCCTTAG	CTGTCTTAAA	GAATGGCAGA	8460
CTGACAGTTG	GTCAGAAGAT	TATTCTTCAT	GGAGCAGAAC	TGGTGGGCTC	TCCTGATGCC	8520
TGTACACCTC	TTGAAGCCCC	AGAATCTCTT	ATGTTAAAGA	TTTCTGCTAA	CAGTACTCGG	8580
CCTGCTCGCT	GGTATACCAA	ACTTGGATTG	TTTCTTGACC	CTAGACCTTT	TCCTCTGCCC	8640
TTATCATCTG	TTTTTCAGTG	TGGAGGAAAT	GTTGGTTGTG	TTGATGTAAT	TATTCAAAGA	8700
GCATACCCTA	TTCAGTGGAT	GGAGAAGACA	TCATCTGGAT	TATACATATT	TCGCAATGAA	8760
AGAGAGGAAG	AAAAGGAAGC	AGCAAAATAT	GTGGAGGCCC	AACAAAAGAG	ACTAGAAGCC	8820
TTATTCACTA	AAATTCAGGA	GGAATTTGAA	GAACATGAAG	AAAACACAAC	AAAACCATAT	8880
TTACCATCAC	GTGACTAAC	AAGACAGCAA	GTTCGTGCTT	TGCAAGATGG	TGCAGAGCTT	8940
TATGAAGCAG	TGAAGAATGC	AGCAGACCCA	GCTTACCTTG	AGGGTTATTT	CAGTGAAGAG	9000
CAGTTAAGAG	CCTTGAATAA	TCACAGGCAA	ATGTTGAATG	ATAAGAAACA	AGCTCAGATC	9060
CAGTTGGAAG	TTAGGAAGGC	CATGGAATCT	GCTGAACAAA	AGGAACAAGG	TTTATCAAGG	9120
GATGTCACAA	CCGTGTGGAA	GTTGCGTATT	GTAAGCTATT	CAAAAAAGA	AAAAGATTCA	9180
GTTATACTGA	GTATTTGGCG	TCCATCATCA	GATTTATATT	CTCTGTTAAC	AGAAGGAAAG	9240
AGATACAGAA	TTTATCATCT	TGCAACTTCA	AAATCTAAAA	GTAAATCTGA	AAGAGCTAAC	9300
ATACAGTTAG	CAGCGACAAA	AAAAACTCAG	TATCAACAAC	TACCGGTTTC	AGATGAAATT	9360
TTATTTTCAGA	TTTACCAGCC	ACGGGAGCCC	CTTCACTTCA	GCAAATTTTT	AGATCCAGAC	9420
TTTCAGCCAT	CTTGTTCTGA	GGTGGACCTA	ATAGGATTTG	TCGTTTCTGT	TGTGAAAAAA	9480
ACAGGACTTG	CCCCTTTCGT	CTATTTGTCA	GACGAATGTT	ACAATTTACT	GGCAATAAAG	9540
TTTTGGATAG	ACCTTAATGA	GGACATTATT	AAGCCTCATA	TGTTAATTGC	TGCAAGCAAC	9600
CTCCAGTGGC	GACCAGAATC	CAAATCAGGC	CTTCTTACTT	TATTTGCTGG	AGATTTTTCT	9660
GTGTTTTCTG	CTAGTCCAAA	AGAGGGCCAC	TTTCAAGAGA	CATTCAACAA	AATGAAAAAT	9720
ACTGTTGAGA	ATATTGACAT	ACTTTGCAAT	GTAGCAGAAA	ACAAGCTTAT	GCATATACTG	9780
CATGCAAAATG	ATCCCAAGTG	GTCCACCCCA	ACTAAAGACT	GTACTTCAGG	GCCGTACACT	9840
GCTCAAATCA	TTCCTGGTAC	AGGAAACAAG	CTTCTGATGT	CTTCTCCTAA	TTGTGAGATA	9900
TATTATCAAA	GTCCTTTATC	ACTTTGTATG	GCCAAAAGGA	AGTCTGTTTC	CACACCTGTC	9960
TCAGCCCAGA	TGACTTCAAA	GTCTTGTAAG	GGGGAGAAAG	AGATTGATGA	CCAAAAGAAC	10020
TGCAAAAAGA	GAAGAGCCTT	GGATTTCTTG	AGTAGACTGC	CTTTACCTCC	ACCTGTTAGT	10080
CCCATTGTA	CATTTGTTTC	TCCGGCTGCA	CAGAAGGCAT	TTCAGCCACC	AAGGAGTTGT	10141

GGCACCAAAT	ACGAAACACC	CATAAAGAAA	AAAGAACTGA	ATTCTCCTCA	GATGACTCCA	10200
TTTAAAAAAT	TCAATGAAAT	TTCTCTTTTG	GAAAGTAATT	CAATAGCTGA	CGAAGAACTT	10260
GCATTGATAA	ATACCCAAGC	TCTTTTGTCT	GGTTCAACAG	GAGAAAAACA	ATTTATATCT	10320
GTCAGTGAAT	CCACTAGGAC	TGCTCCCACC	AGTTCAGAAG	ATTATCTCAG	ACTGAAACGA	10380
CGTTGTACTA	CATCTCTGAT	CAAAGAACAG	GAGAGTTCCC	AGGCCAGTAC	GGAAGAATGT	10440
GAGAAAAATA	AGCAGGACAC	AATTACAAC	AAAAAATATA	TCTAAGCATT	TGCAAAAGGCG	10500
ACAATAAATT	ATTGACGCTT	AACCTTTCCA	GTTTATAAGA	CTGGAATATA	ATTTCAAACC	10560
ACACATTAGT	ACTTATGTTG	CACAATGAGA	AAAGAAATTA	GTTTCAAATT	TACCTCAGCG	10620
TTTGTGTATC	GGGCAAAAAT	CGTTTTGCCC	GATTCCGTAT	TGGTATACTT	TTGCTTCAGT	10680
TGCATATCTT	AAAACTAAAT	GTAATTTATT	AACATAATCAA	GAAAAACATC	TTTGGCTGAG	10740
CTCGGTGGCT	CATGCCTGTA	ATCCCAACAC	TTTGAGAAGC	TGAGGTGGGA	GGAGTGCTTG	10800
AGGCCAGGAG	TTCAAGACCA	GCCTGGGCAA	CATAGGGAGA	CCCCCATCTT	TACGAAGAAA	10860
AAAAAAAAGG	GGAAAAGAAA	ATCTTTTAAA	TCTTTGGATT	TGATCACTAC	AAGTATTATT	10920
TTACAATCAA	CAAAATGGTC	ATCCAAACTC	AAACTTGAGA	AAATATCTTG	CTTTCAAATT	10980
GACACTA						10987